

#6

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.
- (ii) TITLE OF INVENTION: Novel Telomerase
- (iii) NUMBER OF SEQUENCES: 171
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESS: Townsend and Townsend and Crew LLP
  - (B) STREET: Two Embarcadero Center, 8th Floor
  - (C) CITY: San Francisco
  - (D) STATE: California
  - (E) COUNTRY: United States of America
  - (F) ZIP: 94111
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/846,017
  - (B) FILING DATE: 25-APR-1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/844,419
  - (B) FILING DATE: 18-APR-1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/724,643
  - (B) FILING DATE: 01-OCT-1996
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Apple, Randolph T.
  - (B) REGISTRATION NUMBER: 36,429
  - (C) REFERENCE/DOCKET NUMBER: 015389-002920US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (415) 576-0200
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3279 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA	60
TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA	120
TCAAGCTGAT AATCATGGCA TTCACTCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAAGC	180
TAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA	240
TTATAAAGAT TTAGAAGATA TTAAATATT TGCGCAGACA AATATTGTTG CTA CTCCACG	300
AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT CAACTGGACT	360
AATGATCGAA CTTATTGACA AATGCTTAGT TGAAGTTCTT TCATCAAGCG ATGTTTCAGA	420
TAGACAAAAA CTTCAATGAT TTGGATTTC ACTTAAGGGA AATCAATTAG CAAAGACCCA	480
TTTATTAACA GCTCTTTCAA CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT	540
TAGAGCAATG ATTGGAAATG AGCTCTCCG ACATCTCTAC ACTAAATATT TAATATTCCA	600
GCGAAGTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG ATCATTGAA	660
AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG	720
ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT	780
CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT	840
TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT	900
AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA GAATTAGAAA	960
GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT	1020
TAAGTTCAAC TACTATTTAA CAAATCTTG TCCTCTTCCA GAAAATTGGC GGAACGGAA	1080
ACAAAAATC GAAAGTTGA TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA	1140
GCTGTTTAGC TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA	1200
CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC AAAAGAAAGT	1260
TAAGAAATAT GTGGAAGTAA ACAAGCATGA ACTCATTCAC AAAAAGTTAT TGCTTGAGAA	1320
GATCAATACA AGAGAAATAT CATGGATGCA GGTGAGACC TCTGCAAAGC ATTTTATTA	1380
TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT	1440
CGTCGTCTCG CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA	1500
AACCTATTAC TACAGAAAGA ATATTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT	1560
AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT	1620
TGGATTTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT	1680
GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAATTA CTACAAATAC	1740

GAAGTTATTG	AACTCTCACT	TAATGCTTAA	GACATTGAAG	AATAGAATGT	TTAAAGATCC	1800
TTTTGGATTG	GCTGTTTTTA	ACTATGATGA	TGTAATGAAA	AAGTATGAGG	AGTTTGTTTG	1860
CAAATGGAAG	CAAGTTGGAC	AACCAAAACT	CTTCTTTGCA	ACTATGGATA	TCGAAAAGTG	1920
ATATGATAGT	GTAAACAGAG	AAAAACTATC	AACATTCCCTA	AAAACACTA	AATTACTTTC	1980
TTCAGATTTC	TGGATTATGA	CTGCACAAAT	TCTAAAGAGA	AAGAATAACA	TAGTTATCGA	2040
TTGAAAAAC	TTTAGAAAGA	AAGAAATGAA	AGATTATTTT	AGACAGAAAT	TCCAGAAGAT	2100
TGCACTTGAA	GGAGGACAAT	ATCCAACCTT	ATTCAGTGTT	CTTGAAAATG	AACAAAATGA	2160
CTTAAATGCA	AAGAAAACAT	TAATTGTTGA	AGCAAAGCAA	AGAAATTATT	TTAAGAAAGA	2220
TAACCTACTT	CAACCAGTCA	TTAATATTTG	CCAATATAAT	TACATTAACT	TTAATGGGAA	2280
GTTTTATAAA	CAAACAAAAG	GAATTCCTCA	AGGTCTTTGA	GTTTCATCAA	TTTTGTCATC	2340
ATTTTATTAT	GCAACATTAG	AGGAAAGCTC	CTTAGGATTG	CTTAGAGATG	AATCAATGAA	2400
CCCTGAAAAT	CCAAATGTTA	ATCTTCTAAT	GAGACTTACA	GATGACTATC	TTTTGATTAC	2460
AACTCAAGAG	AATAATGCAG	TATTGTTTAT	TGAGAACTT	ATAAACGTAA	GTCGTGAAAA	2520
TGGATTTAAA	TTCAATATGA	AGAAACTACA	GACTAGTTTT	CCATTAAGTC	CAAGCAAATT	2580
TGCAAAATAC	GGAATGGATA	GTGTTGAGGA	GCAAAATATT	GTTCAAGATT	ACTGCGATTG	2640
GATTGGCATC	TCAATTGATA	TGAAAACCTC	TGCTTTAATG	CCAAATATTA	ACTTGAGAAT	2700
AGAAGGAATT	CTGTGTACAC	TCAATCTAAA	CATGCAAACA	AAGAAAGCAT	CAATGTGGCT	2760
CAAGAAGAAA	CTAAAGTCGT	TTTTAATGAA	TAACATTACC	CATTATTTTA	GAAAGACGAT	2820
TACAACCGAA	GACTTTGCGA	ATAAACTCT	CAACAAGTTA	TTTATATCAG	GCGGTTACAA	2880
ATACATGCAA	TGAGCCAAAG	AATACAAGGA	CCACTTTAAG	AAGAACTTAG	CTATGAGCAG	2940
TATGATCGAC	TTAGAGGTAT	CTAAAATTAT	ATACTCTGTA	ACCAGAGCAT	TCTTTAAATA	3000
CCTTGTGTGC	AATATTAAGG	ATACAATTTT	TGGAGAGGAG	CATTATCCAG	ACTTTTTCCT	3060
TAGCACACTG	AAGCACTTTA	TTGAAATATT	CAGCACAAAA	AAGTACATTT	TCAACAGAGT	3120
TTGCATGATC	CTCAAGGCAA	AAGAAGCAAA	GCTAAAAAGT	GACCAATGTC	AATCTCTAAT	3180
TCAATATGAT	GCATAGTCGA	CTATTCTAAC	TTATTTTGGA	AAGTTAATTT	TCAATTTTGG	3240
TCTTATATAC	TGGGGTTTTG	GGGTTTTGGG	GTTTTGGGG			3279

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser  
1 5 10 15  
Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser  
20 25 30  
Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr  
35 40 45  
Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala  
50 55 60  
Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys  
65 70 75 80  
Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu  
85 90 95  
Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln  
100 105 110  
Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu  
115 120 125  
Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp  
130 135 140  
Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr  
145 150 155 160  
Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln  
165 170 175  
Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe  
180 185 190  
Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys  
195 200 205  
Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu  
210 215 220  
Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg  
225 230 235 240  
Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys  
245 250 255  
His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala  
260 265 270  
Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys  
275 280 285  
Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val  
290 295 300  
Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro  
305 310 315 320



Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys  
 325 330 335  
 Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr  
 340 345 350  
 Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn  
 355 360 365  
 Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln  
 370 375 380  
 Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His  
 385 390 395 400  
 Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met  
 405 410 415  
 Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn  
 420 425 430  
 Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val  
 435 440 445  
 Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser  
 450 455 460  
 Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met  
 465 470 475 480  
 Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln  
 485 490 495  
 Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly  
 500 505 510  
 Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr  
 515 520 525  
 Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr  
 530 535 540  
 Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys  
 545 550 555 560  
 Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp  
 565 570 575  
 Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val  
 580 585 590  
 Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr  
 595 600 605  
 Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys  
 610 615 620  
 Leu Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg  
 625 630 635 640  
 Lys Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met  
 645 650 655

Lys Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly  
 660 665 670  
 Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu  
 675 680 685  
 Asn Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe  
 690 695 700  
 Lys Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn  
 705 710 715 720  
 Tyr Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro  
 725 730 735  
 Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr  
 740 745 750  
 Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro  
 755 760 765  
 Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu  
 770 775 780  
 Leu Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu  
 785 790 795 800  
 Ile Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu  
 805 810 815  
 Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met  
 820 825 830  
 Asp Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile  
 835 840 845  
 Gly Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn  
 850 855 860  
 Leu Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr  
 865 870 875 880  
 Lys Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met  
 885 890 895  
 Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe  
 900 905 910  
 Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr  
 915 920 925  
 Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala  
 930 935 940  
 Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val  
 945 950 955 960  
 Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile  
 965 970 975  
 Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His  
 980 985 990

Phe Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys  
 995 1000 1005

Met Ile Leu Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln  
 1010 1015 1020

Ser Leu Ile Gln Tyr Asp Ala  
 1025 1030

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCAAAACC CCAAACCCCC AAAACCCCTA TAAAAAAGA AAAAAATTGAG GTAGTTTAGA	60
AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA TTTGGATGAT ATAGAAAATT	120
TACTTCCTAA TACATTCAAC AAGTATAGCA GCTCTGTAG TGACAAGAAA GGATGCAAAA	180
CATTGAAATC TGGCTCGAAA TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG	240
AGTTCTACTT CTCGGATGCA AATCTTTATA ACGATTCTTT CTGAGAAAA TTAGTTTTAA	300
AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA AATCAGGTAA	360
TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA TTATGGAGAA AATTACTTAA	420
TACTAAAAGG TAAACAGTTT GGATTATTTT CCTAGCCAAC AATGATGAGT ATATTAAATT	480
CATATGAGAA TGAGTCAAAG GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT	540
AAAACGCAAG AAAAAAGTTT ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCG	600
TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC TTGAGACAAT	660
TGAAAAAGCT GTTTACAACT GAAGGAATCG CAGTTCTGAA AGTTCTGATG TGTATGCCAT	720
TATTTTGTGA ATTAATCTCA AATATCTTAT CTCAATTTAA TGGATAGCTA TAGAAACAAA	780
CCAAATAAAC CATGCAAGTT TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC	840
TGAATTTATA TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC	900
TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT AAAAGAAGCA	960
GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT TTGTTGATTC TTCTGTAACC	1020
GGAATTAACA ACAAGAATAT TAGCAACGAA AAAGAAGAAG AGCTATCACA ATCCTGATTC	1080
TTAAAGATTT CAAAATTCC AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG	1140
TTTTTCATTT CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA	1200

GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT TCACATTCAT 1260  
 AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA GCAGTCATCC GTTTTAAAAA 1320  
 TAGTGCTATG AGGACTAAAT TTTTAGAGTC AAGAAATGGA GCCGAAATCT TAATCAAAAA 1380  
 GAATTGCGTC GATATTGCAA AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA 1440  
 ATCTTGATTG ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA 1500  
 GTAACCTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG CGATCTTCAA 1560  
 TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA ATACAAACCT TGGTCAAAAT 1620  
 ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA AAAGAAAAAA TAAGGCAATA AATAAAATGA 1680  
 GTACAGAAGT GAAGAAATAA AAGATTTATT TTTTTCATA ATTTATTGAA AAGAGGGGTT 1740  
 TTGGGGTTTTT GGGGTTTTTG GG 1762

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro Gln Asn Pro Lys Thr Pro Lys Pro Leu Lys Lys Lys Lys Leu Arg  
 1 5 10 15  
 Phe Arg Asn Lys Ile Leu Phe Pro His Lys Trp Arg Trp Ile Leu Ile  
 20 25 30  
 Trp Met Ile Lys Ile Tyr Phe Leu Ile His Ser Thr Ser Ile Ala Ala  
 35 40 45  
 Leu Val Val Thr Arg Lys Asp Ala Lys His Cys Asn Leu Ala Arg Asn  
 50 55 60  
 Arg Leu His Cys Leu Phe Gln Ser Cys Lys Asn Asn Ser Ser Thr Ser  
 65 70 75 80  
 Arg Met Gln Ile Phe Ile Thr Ile Leu Ser Cys Glu Asn Phe Lys Ala  
 85 90 95  
 Glu Ser Lys Glu Lys Leu Lys His Tyr Cys Leu Asn Lys Ile Arg Cys  
 100 105 110  
 Gly Leu Phe Tyr Phe Leu Asp His Phe Leu Arg Ser Ile Met Glu Lys  
 115 120 125  
 Ile Thr Tyr Lys Val Asn Ser Leu Asp Tyr Phe Pro Ser Gln Gln Cys  
 130 135 140  
 Cys Val Tyr Ile His Met Arg Met Ser Gln Arg Ile Ser Ile His Gln  
 145 150 155 160

Thr Tyr Gln Arg Gln Thr Arg Tyr Lys Thr Gln Glu Lys Val Cys Ser  
 165 170 175  
 Asn Ser Arg Arg Thr Tyr Cys Ile Tyr Tyr Ser Tyr Gly Phe Tyr Tyr  
 180 185 190  
 Asn Cys Phe Arg Tyr Arg Arg Cys Thr Pro Glu Ser Cys Asp Asn Cys  
 195 200 205  
 Lys Ser Cys Leu Gln Leu Lys Glu Ser Gln Phe Cys Lys Phe Cys Val  
 210 215 220  
 Cys His Tyr Phe Val Asn Ser Gln Ile Ser Tyr Leu Asn Leu Met Asp  
 225 230 235 240  
 Ser Tyr Arg Asn Lys Pro Asn Lys Pro Cys Lys Phe Asn Gly Ile Tyr  
 245 250 255  
 Val Lys Ser Phe Gly Thr Asn Ala His Cys Ile Tyr Ile Gly Phe Leu  
 260 265 270  
 Lys His Arg Tyr Thr Glu Cys Phe Arg Asp Cys Phe Ser Leu Gln Gln  
 275 280 285  
 Ile Thr Cys Phe Asp Tyr Ser Cys Ser Ser Leu Ile Ser Leu Lys Glu  
 290 295 300  
 Ala Gly Glu Met Lys Arg Arg Leu Lys Lys Glu Ile Ser Lys Phe Val  
 305 310 315 320  
 Asp Ser Ser Val Thr Gly Ile Asn Asn Lys Asn Ile Ser Asn Glu Lys  
 325 330 335  
 Glu Glu Glu Leu Ser Gln Ser Cys Phe Leu Lys Ile Ser Lys Ile Pro  
 340 345 350  
 Gly Lys Arg Asp Thr Phe Ile Lys Ile His Ile Leu Phe Phe Ile Ser  
 355 360 365  
 Gln Leu Leu Phe Ser Phe Ile Leu Thr Ile Phe Phe Asp Leu Glu Val  
 370 375 380  
 Lys Ser Ile Lys Glu Lys Arg Thr Glu Val Thr Leu Ile His Ile His  
 385 390 395 400  
 Arg Ser Thr Phe Ile Tyr Pro Ile Arg Cys Gly Asn Ser Ser His Pro  
 405 410 415  
 Phe Lys Cys Tyr Glu Asp Ile Phe Arg Val Lys Lys Trp Ser Arg Asn  
 420 425 430  
 Leu Asn Gln Lys Glu Leu Arg Arg Tyr Cys Lys Arg Ile Glu Leu Ile  
 435 440 445  
 Phe Arg Val Leu Pro Ile Leu Ile Asp Cys Arg Asp Arg Gly Asn Cys  
 450 455 460  
 Thr Glu Asp His Arg Asn Lys Val Thr Phe Ile Asn Arg Ile Asn Ile  
 465 470 475 480  
 Thr Asn Ile Glu Ile Ser Asp Leu Gln Leu Thr Lys Lys Leu Asn Ser  
 485 490 495

Thr Ile Lys Asn Thr Asn Leu Gly Gln Asn Ile Glu Glu Gly Lys Glu  
500 505 510

Asp Gln Leu Ala Lys Glu Lys Ile Arg Gln Ile Lys Cys Val Gln Lys  
515 520 525

Cys Arg Asn Lys Arg Phe Ile Phe Phe Asn Asn Leu Leu Lys Arg Gly  
530 535 540

Val Leu Gly Phe Trp Gly Phe Gly  
545 550

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Pro Lys Thr Pro Lys Pro Gln Asn Pro Tyr Lys Lys Arg Lys Asn Cys  
1 5 10 15

Gly Ser Leu Glu Ile Lys Tyr Tyr Ser Arg Thr Asn Gly Asp Gly Tyr  
20 25 30

Cys Phe Gly Cys Tyr Arg Lys Phe Thr Ser Tyr Ile Gln Gln Val Gln  
35 40 45

Leu Leu Gln Glu Arg Met Gln Asn Ile Glu Ile Trp Leu Glu Ile Ala  
50 55 60

Phe Ile Asp Tyr Ser Lys Val Ala Lys Thr Ile Arg Val Leu Leu Leu  
65 70 75 80

Gly Cys Lys Ser Leu Arg Phe Phe Leu Glu Lys Ile Ser Phe Lys Lys  
85 90 95

Arg Arg Ala Lys Ser Arg Asn Cys Asn Ile Thr Asn Val Ile Lys Ser  
100 105 110

Gly Asn Glu Asp Tyr Ser Ile Phe Ile Thr Ser Gly Ala Leu Trp Arg  
115 120 125

Lys Leu Leu Asn Thr Lys Arg Thr Val Trp Ile Ile Ser Leu Ala Asn  
130 135 140

Asn Asp Glu Tyr Ile Lys Phe Ile Cys Glu Cys Val Lys Gly Ser Arg  
145 150 155 160

Tyr Ile Arg Leu Thr Lys Asp Lys Leu Ala Ile Lys Arg Lys Lys Lys  
165 170 175

Phe Asp Asn Arg Thr Ala Glu Glu Leu Ile Ala Phe Thr Ile Arg Met  
180 185 190

Gly Phe Ile Thr Ile Val Leu Gly Ile Asp Gly Glu Leu Pro Ser Leu  
195 200 205

Glu Thr Ile Glu Lys Ala Val Tyr Asn Cys Arg Asn Arg Ser Ser Glu  
 210 215 220  
 Ser Ser Asp Val Tyr Ala Ile Ile Leu Cys Ile Asn Leu Lys Tyr Leu  
 225 230 235 240  
 Ile Ser Ile Trp Ile Ala Ile Glu Thr Asn Gln Ile Asn His Ala Ser  
 245 250 255  
 Leu Met Glu Tyr Thr Leu Asn Pro Leu Gly Gln Met His Thr Glu Phe  
 260 265 270  
 Ile Leu Asp Ser Ser Ile Asp Thr Gln Asn Ala Leu Glu Thr Asp Leu  
 275 280 285  
 Ala Tyr Asn Arg Leu Pro Val Leu Ile Thr Leu Ala His Leu Leu Tyr  
 290 295 300  
 Leu Lys Lys Gln Ala Lys Cys Lys Glu Asp Arg Lys Arg Phe Gln Asn  
 305 310 315 320  
 Leu Leu Ile Leu Leu Pro Glu Leu Thr Thr Arg Ile Leu Ala Thr Lys  
 325 330 335  
 Lys Lys Lys Ser Tyr His Asn Pro Asp Ser Arg Phe Gln Lys Phe Gln  
 340 345 350  
 Val Arg Glu Ile His Ser Leu Lys Phe Ile Tyr Tyr Ser Phe Ser Phe  
 355 360 365  
 His Ser Cys Tyr Phe Leu Leu Ser Gln Tyr Phe Leu Ile Ser Trp Lys  
 370 375 380  
 Lys Val Ser Asn Lys Arg Ser Ala Arg Leu Arg Leu Ser Leu Phe Thr  
 385 390 395 400  
 Phe Ile Asp Arg Pro Ser Tyr Ile Gln Tyr Asp Asp Lys Glu Thr Ala  
 405 410 415  
 Val Ile Arg Phe Lys Asn Ser Ala Met Arg Thr Lys Phe Leu Glu Ser  
 420 425 430  
 Arg Asn Gly Ala Glu Ile Leu Ile Lys Lys Asn Cys Val Asp Ile Ala  
 435 440 445  
 Lys Glu Ser Asn Ser Lys Ser Phe Val Asn Lys Tyr Tyr Gln Ser Cys  
 450 455 460  
 Leu Ile Glu Glu Ile Asp Glu Ala Thr Ala Gln Lys Ile Ile Lys Glu  
 465 470 475 480  
 Ile Lys Leu Leu Leu Ile Arg Glu Thr Lys Leu Leu Ile Arg Ser Ala  
 485 490 495  
 Ile Phe Asn Cys Arg Asn Lys Ser Cys Thr Lys Val Arg Gln Lys Ile  
 500 505 510  
 Gln Thr Leu Val Lys Ile Leu Arg Lys Glu Lys Lys Thr Ser Gln Lys  
 515 520 525  
 Lys Lys Gly Asn Lys Asn Glu Tyr Arg Ser Glu Glu Ile Lys Asp Leu  
 530 535 540

Phe Phe Ser Ile Ile Tyr Cys Lys Glu Gly Phe Trp Gly Phe Gly Val  
 545 550 555 560

Leu Gly

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro	Lys	Pro	Gln	Asn	Pro	Lys	Thr	Pro	Ile	Lys	Lys	Glu	Lys	Ile	Glu	1	5	10	15
Val	Val	Lys	Asn	Ile	Ile	Pro	Ala	Gln	Met	Glu	Met	Asp	Ile	Asp	Leu	20	25	30	
Asp	Asp	Ile	Glu	Asn	Leu	Leu	Pro	Asn	Thr	Phe	Asn	Lys	Tyr	Ser	Ser	35	40	45	
Ser	Cys	Ser	Asp	Lys	Lys	Gly	Cys	Lys	Thr	Leu	Lys	Ser	Gly	Ser	Lys	50	55	60	
Ser	Pro	Ser	Leu	Thr	Ile	Pro	Lys	Leu	Gln	Lys	Gln	Leu	Glu	Phe	Tyr	65	70	75	80
Phe	Ser	Asp	Ala	Asn	Leu	Tyr	Asn	Asp	Ser	Phe	Leu	Arg	Lys	Leu	Val	85	90	95	
Leu	Lys	Ser	Gly	Glu	Gln	Arg	Val	Glu	Ile	Glu	Thr	Leu	Leu	Met	Phe	100	105	110	
Lys	Asn	Gln	Val	Met	Arg	Ile	Ile	Leu	Phe	Phe	Arg	Ser	Leu	Leu	Lys	115	120	125	
Glu	His	Tyr	Gly	Glu	Asn	Tyr	Leu	Ile	Leu	Lys	Gly	Lys	Gln	Phe	Gly	130	135	140	
Leu	Phe	Pro	Pro	Thr	Met	Met	Ser	Ile	Leu	Asn	Ser	Tyr	Glu	Asn	Glu	145	150	155	160
Ser	Lys	Asp	Leu	Asp	Thr	Ser	Asp	Leu	Pro	Lys	Thr	Asn	Ser	Leu	Asn	165	170	175	
Ala	Arg	Lys	Ser	Leu	Ile	Ile	Glu	Gln	Gln	Lys	Asn	Leu	Leu	His	Leu	180	185	190	
Leu	Phe	Val	Trp	Val	Leu	Leu	Gln	Leu	Phe	Val	Ser	Thr	Val	Asn	Ser	195	200	205	
Arg	Val	Leu	Arg	Gln	Leu	Lys	Lys	Leu	Phe	Thr	Thr	Glu	Gly	Ile	Ala	210	215	220	
Val	Leu	Lys	Val	Leu	Met	Cys	Met	Pro	Leu	Phe	Cys	Glu	Leu	Ile	Ser	225	230	235	240



Asn Ile Leu Ser Gln Phe Asn Gly Leu Lys Gln Thr Lys Thr Met Gln  
 245 250 255  
 Val Trp Asn Ile Arg Ile Leu Trp Asp Lys Cys Thr Leu Asn Leu Tyr  
 260 265 270  
 Trp Ile Leu Lys Ala Ile His Arg Met Leu Arg Leu Ile Leu Thr Thr  
 275 280 285  
 Asp Tyr Leu Phe Cys Leu Leu Leu Ile Ser Tyr Ile Phe Lys Arg  
 290 295 300  
 Ser Arg Arg Asn Glu Lys Lys Thr Lys Glu Arg Asp Phe Lys Ile Cys  
 305 310 315 320  
 Cys Phe Phe Cys Asn Arg Asn Gln Gln Glu Tyr Gln Arg Lys Arg Arg  
 325 330 335  
 Arg Ala Ile Thr Ile Leu Ile Leu Lys Asp Phe Lys Asn Ser Arg Glu  
 340 345 350  
 Arg Tyr Ile His Asn Ser Tyr Ile Ile Val Phe His Phe Thr Ala Val  
 355 360 365  
 Ile Phe Phe Tyr Leu Asn Asn Ile Phe Cys Leu Ala Gly Ser Lys Lys  
 370 375 380  
 Tyr Gln Ile Arg Glu Ala Leu Asp Cys Gly Asn Leu Ala Tyr Ser His  
 385 390 395 400  
 Ser Ile Asp Leu His Ile Ser Asn Thr Met Ile Arg Lys Gln Gln Ser  
 405 410 415  
 Ser Val Leu Lys Ile Val Leu Cys Gly Leu Asn Phe Ser Gln Glu Met  
 420 425 430  
 Glu Pro Lys Ser Ser Lys Arg Ile Ala Ser Ile Leu Gln Lys Asn Arg  
 435 440 445  
 Thr Leu Asn Leu Ser Leu Ile Ser Ile Thr Asn Leu Asp Cys Leu Lys  
 450 455 460  
 Arg Leu Thr Arg Gln Leu His Arg Arg Ser Leu Lys Lys Ser Asn Phe  
 465 470 475 480  
 Tyr Leu Glu Asn Lys Leu Asn Tyr Tyr Arg Asp Gln Arg Ser Ser Ile  
 485 490 495  
 Asp Glu Ile Lys Ala Glu Leu Lys Leu Asp Asn Lys Lys Tyr Lys Pro  
 500 505 510  
 Trp Ser Lys Tyr Cys Gly Arg Lys Arg Arg Pro Val Ser Lys Arg Lys  
 515 520 525  
 Asn Lys Ala Ile Asn Lys Met Ser Thr Glu Val Lys Lys Lys Ile Tyr  
 530 535 540  
 Phe Phe Gln Phe Ile Glu Lys Arg Gly Phe Gly Val Leu Gly Phe Trp  
 545 550 555 560

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Glu	Ile	Glu	Asn	Asn	Gln	Ala	Gln	Gln	Pro	Lys	Ala	Glu	Lys	Leu	
1				5				10						15		
Trp	Trp	Glu	Leu	Glu	Leu	Glu	Met	Gln	Glu	Asn	Gln	Asn	Asp	Ile	Gln	
		20						25					30			
Val	Arg	Val	Lys	Ile	Asp	Asp	Pro	Lys	Gln	Tyr	Leu	Val	Asn	Val	Thr	
		35					40					45				
Ala	Ala	Cys	Leu	Leu	Gln	Glu	Gly	Ser	Tyr	Tyr	Gln	Asp	Lys	Asp	Glu	
	50					55					60					
Arg	Arg	Tyr	Ile	Ile	Thr	Lys	Ala	Leu	Leu	Glu	Val	Ala	Glu	Ser	Asp	
65					70					75					80	
Pro	Glu	Phe	Ile	Cys	Gln	Leu	Ala	Val	Tyr	Ile	Arg	Asn	Glu	Leu	Tyr	
				85					90					95		
Ile	Arg	Thr	Thr	Thr	Asn	Tyr	Ile	Val	Ala	Phe	Cys	Val	Val	His	Lys	
			100					105						110		
Asn	Thr	Gln	Pro	Phe	Ile	Glu	Lys	Tyr	Phe	Asn	Lys	Ala	Val	Leu	Leu	
		115					120					125				
Pro	Asn	Asp	Leu	Leu	Glu	Val	Cys	Glu	Phe	Ala	Gln	Val	Leu	Tyr	Ile	
		130					135				140					
Phe	Asp	Ala	Thr	Glu	Phe	Lys	Asn	Leu	Tyr	Leu	Asp	Arg	Ile	Leu	Ser	
145					150					155					160	
Gln	Asp	Ile	Arg	Lys	Glu	Leu	Thr	Phe	Arg	Lys	Cys	Leu	Gln	Arg	Cys	
				165					170					175		
Val	Arg	Ser	Lys	Phe	Ser	Glu	Phe	Asn	Glu	Tyr	Gln	Leu	Gly	Lys	Tyr	
			180					185					190			
Cys	Thr	Glu	Ser	Gln	Arg	Lys	Lys	Thr	Met	Phe	Arg	Tyr	Leu	Ser	Val	
		195					200					205				
Thr	Asn	Lys	Gln	Lys	Trp	Asp	Gln	Thr	Lys	Lys	Lys	Arg	Lys	Glu	Asn	
	210					215						220				
Leu	Leu	Thr	Lys	Leu	Gln	Ala	Ile	Lys	Glu	Ser	Glu	Asp	Lys	Ser	Lys	
225					230					235					240	
Arg	Glu	Thr	Gly	Asp	Ile	Met	Asn	Val	Glu	Asp	Ala	Ile	Lys	Ala	Leu	
				245					250					255		
Lys	Pro	Ala	Val	Met	Lys	Lys	Ile	Ala	Lys	Arg	Gln	Asn	Ala	Met	Lys	
			260					265					270			

Lys His Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys  
 275 280 285  
 Tyr Leu Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro  
 290 295 300  
 Lys Glu Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu  
 305 310 315 320  
 Glu Glu Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn  
 325 330 335  
 Pro Glu Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp  
 340 345 350  
 Glu Asn Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn  
 355 360 365  
 Leu Ile Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu  
 370 375 380  
 Ser Asn Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val  
 385 390 395 400  
 Ile Asn Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe  
 405 410 415  
 Pro Leu Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr  
 420 425 430  
 Lys Gly Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln  
 435 440 445  
 Ile Glu Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys  
 450 455 460  
 Asp Met Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn  
 465 470 475 480  
 Glu Gly Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys  
 485 490 495  
 Ile Ala Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile  
 500 505 510  
 Phe Ser Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala  
 515 520 525  
 Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu  
 530 535 540  
 Gly Leu Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe  
 545 550 555 560  
 Ser Ser Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu  
 565 570 575  
 Pro Gly Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys  
 580 585 590  
 Gly Lys Leu Gly Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu  
 595 600 605

Trp Thr Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp  
 610 615 620  
 Met Met Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser  
 625 630 635 640  
 Ile Val Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile  
 645 650 655  
 Lys Ile Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu  
 660 665 670  
 Gly Asp Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser  
 675 680 685  
 Asp Ser Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met  
 690 695 700  
 Val Glu Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly Gln Lys  
 705 710 715

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 872 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu  
 1 5 10 15  
 Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln  
 20 25 30  
 Ile Glu His Tyr Lys Thr Gln Gln Gln Gln Ile Lys Glu Glu Asp Leu  
 35 40 45  
 Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn  
 50 55 60  
 Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu  
 65 70 75 80  
 Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val  
 85 90 95  
 Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys  
 100 105 110  
 Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr  
 115 120 125  
 Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp  
 130 135 140  
 Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg  
 145 150 155 160

Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln  
 165 170 175  
 Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp  
 180 185 190  
 Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val  
 195 200 205  
 Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp  
 210 215 220  
 Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn  
 225 230 235 240  
 Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg  
 245 250 255  
 Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser  
 260 265 270  
 Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu  
 275 280 285  
 Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His  
 290 295 300  
 Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser  
 305 310 315 320  
 Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr  
 325 330 335  
 Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe  
 340 345 350  
 Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro  
 355 360 365  
 Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys  
 370 375 380  
 Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn  
 385 390 395 400  
 Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly  
 405 410 415  
 Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu  
 420 425 430  
 Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr  
 435 440 445  
 Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala  
 450 455 460  
 Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro  
 465 470 475 480  
 Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe  
 485 490 495

Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn  
 500 505 510  
 Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile  
 515 520 525  
 Arg Ser Thr Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met  
 530 535 540  
 Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu  
 545 550 555 560  
 Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His  
 565 570 575  
 Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys  
 580 585 590  
 Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe  
 595 600 605  
 Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu  
 610 615 620  
 Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser  
 625 630 635 640  
 Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu  
 645 650 655  
 Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu  
 660 665 670  
 Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser  
 675 680 685  
 Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe  
 690 695 700  
 Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr  
 705 710 715 720  
 Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln  
 725 730 735  
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu  
 740 745 750  
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln  
 755 760 765  
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln  
 770 775 780  
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser  
 785 790 795 800  
 Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr  
 805 810 815  
 Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn  
 820 825 830

Glu Glu Ile Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu  
835 840 845

Val Lys Ala Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr  
850 855 860

Tyr Asp Tyr Asn Ser Asp Arg Trp  
865 870

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 83 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn Thr Phe Asn  
1 5 10 15

Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys Thr Leu Lys  
20 25 30

Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu Gln Lys Gln  
35 40 45

Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp Ser Phe Leu  
50 55 60

Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu Ile Glu Thr  
65 70 75 80

Leu Leu Met

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn Val Lys Ser Ala Lys Ile Glu Ser Ser Ser Leu Glu Ser Leu Glu  
1 5 10 15

Asp Ile Asp Ser Leu Cys Lys Ser Ile Ala Ser Cys Lys Asn Leu Gln  
20 25 30

Asn Val Asn Ile Ile Ala Ser Leu Leu Tyr Pro Asn Asn Ile Gln Lys  
35 40 45

Asn Pro Phe Asn Lys Pro Asn Leu Leu Phe Phe Lys Gln Phe Glu Gln  
50 55 60

Leu Lys Asn Leu Glu Asn Val Ser Ile Asn Cys Ile Leu Asp Gln His  
65 70 75 80  
Ile Leu Asn Ser Ile Ser Glu Phe Leu Glu Lys Asn Lys Lys Ile Lys  
85 90 95  
Ala Phe Ile Leu  
100

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 85 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Met Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn  
1 5 10 15  
Thr Phe Asn Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys  
20 25 30  
Thr Leu Lys Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu  
35 40 45  
Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp  
50 55 60  
Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu  
65 70 75 80  
Ile Glu Thr Leu Leu  
85

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 98 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ile Glu Leu Ala Ile Lys Ile Ala Val Asn Lys Asn Leu Asp Glu Ile  
1 5 10 15  
Lys Gly His Thr Ala Ile Phe Ser Asp Val Ser Gly Ser Met Ser Thr  
20 25 30  
Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu  
35 40 45  
Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg Cys Glu Lys  
50 55 60



Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys Lys Cys Tyr  
65 70 75 80  
Leu Glu Val Asp Leu Pro Gly Asp Glu Leu Arg Pro Ser Met Gln Lys  
85 90 95  
Leu Leu

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr  
1 5 10 15  
Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys  
20 25 30  
Leu Leu Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys  
35 40 45  
Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser  
50 55 60  
Ser Leu Gly Phe Leu  
65

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Asn Arg Asn Leu His Cys Thr Tyr Ile Asp Tyr Lys Lys Ala Phe  
1 5 10 15  
Asp Ser Ile Pro His Ser Trp Leu Ile Gln Val Leu Glu Ile Tyr Lys  
20 25 30  
Ile Asn Arg Gln Ile Ala Ile Lys Lys Gly Ile Tyr Gln Gly Asp Ser  
35 40 45  
Leu Ser Pro Leu Trp Phe Cys Leu Ala Leu Asn Pro Leu Ser His Gln  
50 55 60  
Leu His Asn Asp Arg  
65

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Gly Gly Ser Asn Trp Phe Arg Glu Val Asp Leu Lys Lys Cys Phe  
1 5 10 15  
Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile  
20 25 30  
Ser Asp His Val Pro Val Gly Pro Arg Val Cys Val Gln Gly Ala Pro  
35 40 45  
Thr Ser Pro Ala Leu Cys Asn Ala Val Leu Leu Arg Leu Asp Arg Arg  
50 55 60  
Leu Ala Gly Leu Ala  
65

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr  
1 5 10 15  
Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr  
20 25 30  
Ile Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys  
35 40 45  
Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro  
50 55 60  
Phe Arg Lys Gln Asn  
65

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 69 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: not relevant  
    (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Val Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr
1          5          10          15
Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys Asp Ala Leu
20          25          30
Lys Asn Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser
35          40          45
Leu Ser Ala Pro Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe
50          55          60
Tyr Ser Glu Phe Lys
65
```

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: not relevant  
    (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu Asn
1          5          10          15
Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu Asn
20          25          30
Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Gln Asp Tyr Cys Asp
35          40          45
Trp Ile Gly Ile Ser Ile
50
```

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: not relevant  
    (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

His Leu Ile Tyr Met Asp Asp Ile Lys Leu Tyr Ala Lys Asn Asp Lys  
1 5 10 15  
Glu Met Lys Lys Leu Ile Asp Thr Thr Thr Ile Phe Ser Asn Asp Ile  
20 25 30  
Ser Met Gln Phe Gly Leu Asp Lys Cys Lys Thr Lys Cys Leu Tyr Lys  
35 40 45  
Tyr Leu Gly Phe Gln Gln  
50

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Val Arg Tyr Ala Asp Asp Ile Leu Ile Gly Val Leu Gly Ser Lys  
1 5 10 15  
Asn Lys Ile Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly  
20 25 30  
Leu Thr Ile Asn Glu Glu Lys Thr Leu Ile Glu Thr Pro Ala Arg Phe  
35 40 45  
Leu Gly Tyr Asn Ile  
50

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser His Leu Glu Ile  
1 5 10 15  
Gly His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp  
20 25 30  
Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu  
35 40 45  
Trp Met Gly Tyr Glu Leu  
50

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 49 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: not relevant  
    (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln  
1                    5                    10                    15  
Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr  
                    20                    25                    30  
Asn Ala Lys Ala Asn Arg Ile Arg Ser Lys Ser Ser Lys Gly Ile Phe  
                    35                    40                    45  
Arg

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 39 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: not relevant  
    (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn  
1                    5                    10                    15  
Asp Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val  
                    20                    25                    30  
Glu Ile Glu Thr Leu Leu Met  
                    35

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 37 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: not relevant  
    (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile Cys His Gln Glu Tyr Tyr Phe Gly Asp Phe Asn Leu Pro Arg Asp  
1 5 10 15  
Lys Phe Leu Lys Glu Gln Ile Lys Leu Asp Glu Gly Trp Val Pro Leu  
20 25 30  
Glu Ile Met Ile Lys  
35

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile Cys Glu Gln Ile Glu Tyr Tyr Phe Gly Asp His Asn Leu Pro Arg  
1 5 10 15  
Asp Lys Phe Leu Lys Gln Gln Ile Leu Leu Asp Asp Gly Trp Val Pro  
20 25 30  
Leu Glu Thr Met Ile Lys  
35

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile Leu Arg Gln Val Glu Tyr Tyr Phe Gly Asp Ala Asn Leu Asn Arg  
1 5 10 15  
Asp Lys Phe Leu Arg Glu Gln Ile Gly Lys Asn Glu Asp Gly Trp Val  
20 25 30  
Pro Leu Ser Val Leu Val Thr  
35

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys Leu Lys Gln Val Glu Phe Tyr Phe Ser Glu Phe Asn Phe Pro Tyr  
1 5 10 15  
Asp Arg Phe Leu Arg Thr Thr Ala Glu Lys Asn Asp Gly Trp Val Pro  
20 25 30  
Ile Ser Thr Ile Ala Thr  
35

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TAGACCTGTT AGTGTACATT TGAATTGAAG C

31

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAGACCTGTT AGGTTGGATT TGTGGCATCA

30

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAAAACCCCA AAACCTAACA GGTCTA

26

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 103 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCGGGAATTC TAATACGACT CACTATAGGG AAGAACTCT GATGAGGCCG AAAGGCCGAA 60  
ACTCCACGAA AGTGGAGTAA GTTTCTCGAT AATTGATCTG TAG 103

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGGGATCCT CTTCAAAGA TGAGAGGACA GCAAAC 36

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCCCAAAACC CCAAACCCC AAAACCCCA CAGGGGTTTT GGGGTTTTGG GGTTTTGGGG 60

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCAAAACCCC AAAACCCCAA AACCCCAACA GGGGTTTTGG GGTTTTGGGG TTTTGGGG 58



(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAAACCCCAA AACCCCAAAA CCCCACAGG GGTTTGGGG TTTTGGGGTT TTGGGG

56

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AACCCCAAAA CCCCAAACC CCCACAGGG TTTTGGGGTT TTGGGGTTTT GGGG

54

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCCCAAAACC CCAAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAAACCCCAA AACCCCAAAA CCCCACAGG GGTTTGGGG TTTTGGGGTT TT

52

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACCCCAAAA CCCCAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT

50

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 48 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCCCAAAACC CCAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 46 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCAAAACCCC.AAAACCCCCA CAGGGGTTTT GGGGTTTTGG GGTTTT

46

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 44 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAAACCCCAA AACCCCCACA GGGGTTTTGG GGTTTTGGGG TTTT

44

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "RNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTTGGGG

8

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "RNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGGGTTTT

8

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCTRAARTAR TGDGTNADRT TRTTCAT

27

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCGGATCCAT GAAYCCWGAR AAYCCWAAYG T

31

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

NNNGTNACHG GHATHAAYAA

20

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

DGCDGTYTCY TGRTCRTTTRT A

21

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2421 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AACTCATTTA ATTACTAATT TAATCAACAA GATTGATAAA AAGCAGTAAA TAAAACCCAA	60
TAGATTTAAT TTAGAAAGTA TCAATTGAAA AATGGAAATT GAAAACAAC T AAGCACAATA	120
GCCAAAAGCC GAAAAATTGT GGTGGGAACT TGAATTAGAG ATGCAAGAAA ACCAAAAATGA	180
TATATAAGTT AGGGTTAAGA TTGACGATCC TAAGCAATAT CTCGTGAACG TCACTGCAGC	240
ATGTTTGTTG TAGGAAGGTA GTTACTACTA AGATAAAGAT GAAAGAAGAT ATATCATCAC	300
TAAAGCACTT CTTGAGGTGG CTGAGTCTGA TCCTGAGTTC ATCTGCTAGT TGGCAGTCTA	360
CATCCGTAAT GAACTTTACA TCAGAACTAC CACTAACTAC ATTGTAGCAT TTTGTGTTGT	420
CCACAAGAAT ACTCAACCAT TCATCGAAAA GTACTTCAAC AAAGCAGTAC TTTTGCCTAA	480
TGACTTACTG GAAGTCTGTG AATTTGCATA GGTTCTCTAT ATTTTTGATG CAACTGAATT	540
CAAAAATTTG TATCTTGATA GGATACTTTC ATAAGATATT CGTAAGGAAC TCACTTTCCG	600
TAAGTGTTTA CAAAGATGCG TCAGAAGCAA GTTTTCTGAA TTCAACGAAT ACTAACTTGG	660
TAAGTATTGC ACTGAATCCT AACGTAAGAA AACAATGTTC CGTTACCTCT CAGTTACCAA	720
CAAGTAAAAG TGGGATTAAA CTAAGAAGAA GAGAAAAGAG AATCTCTTAA CCAAACTTTA	780
GGCAATAAAG GAATCTGAAG ATAAGTCCAA GAGAGAAACT GGAGACATAA TGAACGTTGA	840
AGATGCAATC AAGGCTTTAA AACCAGCAGT TATGAAGAAA ATAGCCAAGA GATAGAATGC	900
CATGAAGAAA CACATGAAGG CACCTAAAT TCCTAACTCT ACCTTGGAAT CAAAGTACTT	960
GACCTTCAAG GATCTCATTA AGTTCTGCCA TATTTCTGAG CCTAAAGAAA GAGTCTATAA	1020
GATCCTTGGT AAAAAATACC CTAAGACCGA AGAGGAATAC AAAGCAGCCT TTGGTGATTC	1080
TGCATCTGCA CCCTTCAATC CTGAATTGGC TGGAAAGCGT ATGAAGATTG AAATCTCTAA	1140
AACATGGGAA AATGAACTCA GTGCAAAAGG CAACACTGCT GAGGTTTGGG ATAATTTAAT	1200
TTCAAGCAAT TAACTCCCAT ATATGGCCAT GTTACGTAAC TTGTCTAACA TCTTAAAAGC	1260
CGGTGTTTCA GATACTACAC ACTCTATTGT GATCAACAAG ATTTGTGAGC CCAAGGCCGT	1320
TGAGAACTCC AAGATGTTCC CTCTTCAATT CTTTAGTGCC ATTGAAGCTG TTAATGAAGC	1380
AGTTACTAAG GGATTCAAGG CCAAGAAGAG AGAAAATATG AATCTTAAAG GTCAAATCGA	1440
AGCAGTAAAG GAAGTTGTTG AAAAAACCGA TGAAGAGAAG AAAGATATGG AGTTGGAGTA	1500

AACCGAAGAA GGAGAATTTG TTAAAGTCAA CGAAGGAATT GGCAAGCAAT ACATTAAGTC 1560  
 CATTGAACTT GCAATCAAGA TAGCAGTTAA CAAGAATTTA GATGAAATCA AAGGACACAC 1620  
 TGCAATCTTC TCTGATGTTT CTGGTTCTAT GAGTACCTCA ATGTCAGGTG GAGCCAAGAA 1680  
 GTATGGTTCC GTTCGTACTT GTCTCGAGTG TGCATTAGTC CTTGGTTTGA TGGTAAAATA 1740  
 ACGTTGTGAA AAGTCCTCAT TCTACATCTT CAGTTCACCT AGTTCTCAAT GCAATAAGTG 1800  
 TTAAGTAGAA GTTGATCTCC CTGGAGACGA ACTCCGTCCT TCTATGTAAA AACTTTTGCA 1860  
 AGAGAAAGGA AAAGTTGGTG GTGGTACTGA TTTCCCTAT GAGTGCATTG ATGAATGGAC 1920  
 AAAGAATAAA ACTCACGTAG ACAATATCGT TATTTTGTCT GATATGATGA TTGCAGAAAG 1980  
 ATATTCAGAT ATCAATGTGA GAGGCAGTTC CATTGTTAAC AGCATCAAAA AGTACAAGGA 2040  
 TGAAGTAAAT CCTAACATTA AAATCTTTC AGTTGACTTA GAAGGTTACG GAAAGTGCCT 2100  
 TAATCTAGGT GATGAGTTCA ATGAAAACAA CTACATCAAG ATATTCGGTA TGAGCGATTC 2160  
 AATCTTAAAG TTCATTTTCAG CCAAGCAAGG AGGAGCAAAT ATGGTCGAAG TTATCAAAAA 2220  
 CTTTGCCCTT CAAAAAATAG GACAAAAGTG AGTTTCTTGA GATTCTTCTA TAACAAAAAT 2280  
 CTCACCCAC TTTTTTGTTC TATTGCATAG CCATTATGAA ATTTAAATTA TTATCTATTT 2340  
 ATTTAAGTTA CTTACATAGT TTATGTATCG CAGTCTATTA GCCTATTCAA ATGATTCTGC 2400  
 AAAGAACAAA AAAGATTAAA A 2421

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Glu Leu Glu Leu Glu Met Gln Glu Asn Gln Asn Asp Ile Gln Val Arg  
 1 5 10 15  
 Val Lys Ile Asp Asp Pro Lys Gln Tyr Leu Val Asn Val Thr Ala Ala  
 20 25 30  
 Cys Leu Leu Gln Glu Gly Ser Tyr Tyr Gln Asp Lys Asp Glu Arg Arg  
 35 40 45  
 Tyr Ile Ile Thr Lys Ala Leu Leu Glu Val Ala Glu Ser Asp Pro Glu  
 50 55 60  
 Phe Ile Cys Gln Leu Ala Val Tyr Ile Arg Asn Glu Leu Tyr Ile Arg  
 65 70 75 80  
 Thr Thr Thr Asn Tyr Ile Val Ala Phe Cys Val Val His Lys Asn Thr  
 85 90 95

Gln Pro Phe Ile Glu Lys Tyr Phe Asn Lys Ala Val Leu Leu Pro Asn  
 100 105 110  
 Asp Leu Leu Glu Val Cys Glu Phe Ala Gln Val Leu Tyr Ile Phe Asp  
 115 120 125  
 Ala Thr Glu Phe Lys Asn Leu Tyr Leu Asp Arg Ile Leu Ser Gln Asp  
 130 135 140  
 Ile Arg Lys Glu Leu Thr Phe Arg Lys Cys Leu Gln Arg Cys Val Arg  
 145 150 155 160  
 Ser Lys Phe Ser Glu Phe Asn Glu Tyr Gln Leu Gly Lys Tyr Cys Thr  
 165 170 175  
 Glu Ser Gln Arg Lys Lys Thr Met Phe Arg Tyr Leu Ser Val Thr Asn  
 180 185 190  
 Lys Gln Lys Trp Asp Gln Thr Lys Lys Lys Arg Lys Glu Asn Leu Leu  
 195 200 205  
 Thr Lys Leu Gln Ala Ile Lys Glu Ser Glu Asp Lys Ser Lys Arg Glu  
 210 215 220  
 Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu Lys Pro  
 225 230 235 240  
 Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys Lys His  
 245 250 255  
 Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys Tyr Leu  
 260 265 270  
 Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro Lys Glu  
 275 280 285  
 Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu Glu Glu  
 290 295 300  
 Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn Pro Glu  
 305 310 315 320  
 Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp Glu Asn  
 325 330 335  
 Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn Leu Ile  
 340 345 350  
 Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu Ser Asn  
 355 360 365  
 Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val Ile Asn  
 370 375 380  
 Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe Pro Leu  
 385 390 395 400





(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCAATACTAT TAATTAATAA ATAAAAAATAA GCAAACTACA AAGAAAATGT CAAGGCGTAA	60
CTAAAAAAG CCATAGGCTC CTATAGGCAA TGAAACAAAT CTTGATTTTG TATTACAAAA	120
TCTAGAAGTT TACAAAAGCC AGATTGAGCA TTATAAGACC TAGTAGTAAT AGATCAAAGA	180
GGAGGATCTC AAGCTTTTAA AGTTCAAAAA TTAAGATTAG GATGGAAACT CTGGCAACGA	240
TGATGATGAT GAAGAAAACA ACTCAAATAA ATAATAAGAA TTATTAAGGA GAGTCAATTA	300
GATTAAGTAG CAAGTTTAAT TGATAAAAAA AGTTGGTTCT AAGGTAGAGA AAGATTTGAA	360
TTTGAACGAA GATGAAACA AAAAGAATGG ACTTTCTGAA TAGCAAGTGA AAGAAGAGTA	420
ATTAAGAACG ATTACTGAAG AATAGGTTAA GTATTAAAAT TTAGTATTTA ACATGGACTA	480
CCAGTTAGAT TTAAATGAGA GTGGTGGCCA TAGAAGACAC AGAAGAGAAA CAGATTATGA	540
TACTGAAAAA TGGTTTGAAA TATCTCATGA CCAAAAAAAT TATGTATCAA TTTACGCCAA	600
CTAAAAGACA TCATATTGTT GGTGGCTTAA AGATTATTTT AATAAAAAACA ATTATGATCA	660
TCTTAATGTA AGCATTAAAC GACTAGAAAC TGAAGCCGAA TTCTATGCCT TTGATGATTT	720
TTCAACAAACA ATCAAACTTA CTAATAATTC TTACTAGACT GTTAACATAG ACGTTAATTT	780
TGATAATAAT CTCTGTATAC TCGCATTGCT TAGATTTTTA TTATCACTAG AAAGATTCAA	840
TATTTTGAAT ATAAGATCTT CTTATACAAG AAATTAATAT AATTTTGAGA AAATTGGTGA	900
GCTACTTGAA ACTATCTTCG CAGTTGTCTT TTCTCATCGC CACTTACAAG GCATTCATTT	960
ACAAGTTCCT TCGGAAGCGT TCTAATATTT AGTTAACTCC TCATCATAAA TTAGCGTTAA	1020
AGATAGCTAA TTATAGGTAT ACTCTTTCTC TACAGACTTA AAATTAGTTG AACTAACAA	1080
AGTCCAAGAT TATTTTAAGT TCTTATAAGA ATTCCCTCGT TTGACTCATG TAAGCTAGTA	1140
GGCTATCCCA GTTAGTGCTA CTAACGCTGT AGAGAACCTC AATGTTTTAC TTAAAAGGT	1200
CAAGCATGCT AATCTTAATT TAGTTTCTAT CCCTACCTAA TTCAATTTTG ATTTCTACTT	1260
TGTTAATTTA TAACATTTGA AATTAGAGTT TGGATTAGAA CCAAATATTT TGACAAAACA	1320
AAAGCTTGAA AATCTACTTT TGAGTATAAA ATAATCAAAA AATCTTAAAT TTTTAAGATT	1380
AACTTTTAC ACCTACGTTG CTTAAGAAAC CTCCAGAAAA CAGATATTAA AACAAGCTAC	1440
AACAATCAAA AATCTCAAAA ACAATAAAAA TCAAGAAGAA ACTCCTGAAA CTAAAGATGA	1500
AACTCCAAGC GAAAGCACAA GTGGTATGAA ATTTTTTGAT CATCTTTCTG AATTAACCGA	1560
GCTTGAAGAT TTCAGCGTTA ACTTGTAAGC TACCCAAGAA ATTTATGATA GCTTGACAA	1620

ACTTTTGATT AGATCAACAA ATTTAAAGAA GTTCAAATTA AGTTACAAAT ATGAAATGGA 1680  
 AAAGAGTAAA ATGGATACAT TCATAGATCT TAAGAATATT TATGAAACCT TAAACAATCT 1740  
 TAAAAGATGC TCTGTTAATA TATCAAATCC TCATGGAAAC ATTTCTTATG AACTGACAAA 1800  
 TAAAGATTCT ACTTTTTATA AATTTAAGCT GACCTTAAAC TAAGAATTAT AACACGCTAA 1860  
 GTATACTTTT AAGTAGAACG AATTTTAATT TAATAACGTT AAAAGTGCAA AAATTGAATC 1920  
 TTCCTCATTG GAAAGCTTAG AAGATATTGA TAGTCTTTGC AAATCTATTG CTTCTTGTA 1980  
 AAATTTACAA AATGTTAATA TTATCGCCAG TTTGCTCTAT CCCAACAATA TTTAGAAAAA 2040  
 TCCTTTCAAT AAGCCCAATC TTCTATTTTT CAAGCAATTT GAATAATTGA AAAATTTGGA 2100  
 AAATGTATCT ATCAACTGTA TTCTTGATCA GCATATACTT AATTCTATTT CAGAATTCTT 2160  
 AGAAAAGAAT AAAAAAATAA AAGCATTCTT TTTGAAAAGA TATTATTTAT TACAATATTA 2220  
 TCTTGATTAT ACTAAATTAT TTAAACACT TCAATAGTTA CCTGAATTAA ATTAAGTTTA 2280  
 CATTAATTAG CAATTAGAAG AATTGACTGT GAGTGAAGTA CATAAGTAAG TATGGGAAAA 2340  
 CCACAAGCAA AAAGCTTTCT ATGAACCATT ATGTGAGTTT ATCAAAGAAT CATCCTAAAC 2400  
 CCTTTAGCTA ATAGATTTTG ACCAAAACAC TGTAAGTGAT GACTCTATTA AAAAGATTTT 2460  
 AGAATCTATA TCTGAGTCTA AGTATCATCA TTATTTGAGA TTGAACCCTA GTTAATCTAG 2520  
 CAGTTTAATT AAATCTGAAA ACGAAGAAAT TTAAGAACTT CTCAAAGCTT GCGACGAAAA 2580  
 AGGTGTTTTA GTAAAAGCAT ACTATAAATT CCCTCTATGT TTACCAACTG GTACTTATTA 2640  
 CGATTACAAT TCAGATAGAT GGTGATTAAT TAAATATTAG TTTAAATAAA TATTAAATAT 2700  
 TGAATATTC TTTGCTTATT ATTTGAATAA TACATACAAT AGTCATTTTT AGTGTTTTGA 2760  
 ATATATTTTA GTTATTTAAT TCATTATTTT AAGTAAATAA TTATTTTCA ATCATTTTTT 2820  
 AAAAAATCG 2829

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Ser	Arg	Arg	Asn	Gln	Lys	Lys	Pro	Gln	Ala	Pro	Ile	Gly	Asn	Glu
1				5				10					15		
Thr	Asn	Leu	Asp	Phe	Val	Leu	Gln	Asn	Leu	Glu	Val	Tyr	Lys	Ser	Gln
	20						25						30		
Ile	Glu	His	Tyr	Lys	Thr	Gln	Gln	Gln	Ile	Lys	Glu	Glu	Asp	Leu	
	35					40					45				

Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn  
 50 55 60  
 Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu  
 65 70 75 80  
 Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val  
 85 90 95  
 Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys  
 100 105 110  
 Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr  
 115 120 125  
 Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp  
 130 135 140  
 Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg  
 145 150 155 160  
 Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln  
 165 170 175  
 Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp  
 180 185 190  
 Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val  
 195 200 205  
 Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp  
 210 215 220  
 Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn  
 225 230 235 240  
 Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg  
 245 250 255  
 Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser  
 260 265 270  
 Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu  
 275 280 285  
 Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His  
 290 295 300  
 Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser  
 305 310 315 320  
 Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr  
 325 330 335  
 Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe  
 340 345 350  
 Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro  
 355 360 365  
 Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys  
 370 375 380

Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn  
385 390 395 400  
Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly  
405 410 415  
Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu  
420 425 430  
Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr  
435 440 445  
Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala  
450 455 460  
Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro  
465 470 475 480  
Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe  
485 490 495  
Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn  
500 505 510  
Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile  
515 520 525  
Arg Ser Thr Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met  
530 535 540  
Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu  
545 550 555 560  
Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His  
565 570 575  
Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys  
580 585 590  
Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe  
595 600 605  
Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu  
610 615 620  
Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser  
625 630 635 640  
Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu  
645 650 655  
Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu  
660 665 670  
Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser  
675 680 685  
Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe  
690 695 700  
Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr  
705 710 715 720

Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln  
 725 730 735  
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu  
 740 745 750  
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln  
 755 760 765  
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln  
 770 775 780  
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser  
 785 790 795 800  
 Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr  
 805 810 815  
 Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn  
 820 825 830  
 Glu Glu Ile Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu  
 835 840 845  
 Val Lys Ala Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr  
 850 855 860  
 Tyr Asp Tyr Asn Ser Asp Arg Trp  
 865 870

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu  
 1 5 10 15  
 Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn  
 20 25 30  
 Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg  
 35 40 45  
 Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val  
 50 55 60  
 Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn  
 65 70 75 80  
 Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn  
 85 90 95  
 Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly  
 100 105 110

Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val  
 115 120 125  
 Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe  
 130 135 140  
 Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys  
 145 150 155 160  
 Trp Val Gln Arg Ser Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys  
 165 170 175  
 Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn  
 180 185 190  
 Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser  
 195 200 205  
 Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr  
 210 215 220  
 Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr  
 225 230 235 240  
 Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile  
 245 250 255  
 Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser  
 260 265 270  
 His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile  
 275 280 285  
 Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys  
 290 295 300  
 Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Ser Leu Pro  
 305 310 315 320  
 Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu  
 325 330 335  
 Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His  
 340 345 350  
 Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu  
 355 360 365  
 Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr  
 370 375 380  
 Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp  
 385 390 395 400  
 Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu  
 405 410 415  
 Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn  
 420 425 430  
 Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu  
 435 440 445

Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe  
 450 455 460  
 Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys  
 465 470 475 480  
 Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile  
 485 490 495  
 Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg  
 500 505 510  
 Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys  
 515 520 525  
 Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met  
 530 535 540  
 Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg  
 545 550 555 560  
 Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn  
 565 570 575  
 Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp  
 580 585 590  
 Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val  
 595 600 605  
 Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr  
 610 615 620  
 Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile  
 625 630 635 640  
 Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys  
 645 650 655  
 Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe  
 660 665 670  
 Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu  
 675 680 685  
 Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys  
 690 695 700  
 Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe  
 705 710 715 720  
 Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser  
 725 730 735  
 Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile  
 740 745 750  
 Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr  
 755 760 765  
 Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp  
 770 775 780

His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp  
 785 790 795 800  
 Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln  
 805 810 815  
 Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp  
 820 825 830  
 Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu  
 835 840 845  
 Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu  
 850 855 860  
 Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile  
 865 870 875 880  
 His Ile Val Asn

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

DGTDATNARN ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:



Leu Cys Val Ser Tyr Ile Leu Ser Ser Phe Tyr Tyr Ala Asn Leu Glu  
 1 5 10 15  
 Glu Asn Ala Leu Gln Phe Leu Arg Lys Glu Ser Met Asp Pro Glu Lys  
 20 25 30  
 Pro Glu Thr Asn Leu Leu Met Arg Leu Thr  
 35 40

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu  
 1 5 10 15  
 Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn  
 20 25 30  
 Pro Asn Val Asn Leu Leu Met Arg Leu Thr  
 35 40

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "RNA"

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
  - (B) LOCATION: 12..25
  - (D) OTHER INFORMATION: /mod\_base= OTHER
- /note= "The residues located at these positions are 2-O-methylribonucleoti..."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TAGACCTGTT AGGUUUUGGG GUUUUG

26

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGGGTTTTGG GGT

16

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: /note= "expressed sequence tag (EST)  
AA281296"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCCAAGTTCC TGC	ACTGGCT	GATGAGTGTG	TACGTCGTCG	AGCTGCTCAG	GTCTTTCTTT	60
TATGTCACGG	AGACCACGTT	TCAAAAGAAC	AGGCTCTTTT	TCTACCGGAA	GAGTGTCTGG	120
AGCAAGTTGC	AAAGCATTGG	AATCAGACAG	CACTTGAAGA	GGGTGCAGCT	GCGGGACGTG	180
TCGGAAGCAG	AGGTCAGGCA	GCATCGGGAA	GCCAGGCCCG	CCCTGCTGAC	GTCCAGACTC	240
CGCTTCATCC	CCAAGCCTGA	CGGGCTGCGG	CCGATTGTGA	ACATGGACTA	CGTCGTGGGA	300
GCCAGAACGT	TCCGCAGAGA	AAAGAGGGCC	GAGCGTCTCA	CCTCGAGGGT	GAAGGCACTG	360
TTCAGCGTGC	TCAACTACGA	GCGGGCGCG				389

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from  
Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile	Ser	Glu	Ile	Glu	Trp	Leu	Val	Leu	Gly	Lys	Arg	Ser	Asn	Ala	Lys
1				5					10					15	
Met	Cys	Leu	Ser	Asp	Phe	Glu	Lys	Arg	Lys	Gln	Ile	Phe	Ala	Glu	Phe
			20					25					30		

Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe  
 35 40 45  
 Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe  
 50 55 60  
 Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met  
 65 70 75 80  
 Lys Met Glu Ala Phe Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp  
 85 90 95  
 Thr Gln Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys  
 100 105 110  
 Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile  
 115 120 125  
 Lys Met Gly Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu  
 130 135 140  
 Arg Pro Val Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser  
 145 150 155 160  
 Gly Ile Pro Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys  
 165 170 175  
 Lys Asp Leu Leu Lys His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val  
 180 185 190  
 Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met  
 195 200 205  
 Phe Arg Ile Val Lys Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg  
 210 215 220  
 Lys Tyr Ala Thr Ile His Ala Thr Ser  
 225 230

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from *Saccharomyces cerevisiae* EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Leu Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys  
 1 5 10 15

His Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp  
                   20                                  25                                  30  
 Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys  
                   35                                  40                                  45  
 Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr  
                   50                                  55                                  60  
 Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr  
                   65                                  70                                  75                                  80  
 Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser  
                                   85                                  90                                  95  
 Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn  
                                   100                                  105                                  110  
 Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu  
                   115                                  120                                  125  
 Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln  
                   130                                  135                                  140  
 Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys  
                   145                                  150                                  155                                  160  
 Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln  
                                   165                                  170                                  175  
 Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met  
                                   180                                  185                                  190  
 Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys  
                   195                                  200                                  205  
 Met Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val  
                   210                                  215                                  220  
 Arg Ser Gln Tyr Phe Phe Asn Thr Asn  
                   225                                  230

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr	Arg	Glu	Ile	Ser	Trp	Met	Gln	Val	Glu	Thr	Ser	Ala	Lys	His	Phe	1	5	10	15
Tyr	Tyr	Phe	Asp	His	Glu	Asn	Ile	Tyr	Val	Leu	Trp	Lys	Leu	Leu	Arg	20	25	30	
Trp	Ile	Phe	Glu	Asp	Leu	Val	Val	Ser	Leu	Ile	Arg	Cys	Phe	Phe	Tyr	35	40	45	
Val	Thr	Glu	Gln	Gln	Lys	Ser	Tyr	Ser	Lys	Thr	Tyr	Tyr	Tyr	Arg	Lys	50	55	60	
Asn	Ile	Trp	Asp	Val	Ile	Met	Lys	Met	Ser	Ile	Ala	Asp	Leu	Lys	Lys	65	70	75	80
Glu	Thr	Leu	Ala	Glu	Val	Gln	Glu	Lys	Glu	Val	Glu	Glu	Trp	Lys	Lys	85	90	95	
Ser	Leu	Gly	Phe	Ala	Pro	Gly	Lys	Leu	Arg	Leu	Ile	Pro	Lys	Lys	Thr	100	105	110	
Thr	Phe	Arg	Pro	Ile	Met	Thr	Phe	Asn	Lys	Lys	Ile	Val	Asn	Ser	Asp	115	120	125	
Arg	Lys	Thr	Thr	Lys	Leu	Thr	Thr	Asn	Thr	Lys	Leu	Leu	Asn	Ser	His	130	135	140	
Leu	Met	Leu	Lys	Thr	Leu	Lys	Asn	Arg	Met	Phe	Lys	Asp	Pro	Phe	Gly	145	150	155	160
Phe	Ala	Val	Phe	Asn	Tyr	Asp	Asp	Val	Met	Lys	Lys	Tyr	Glu	Glu	Phe	165	170	175	
Val	Cys	Lys	Trp	Lys	Gln	Val	Gly	Gln	Pro	Lys	Leu	Phe	Phe	Ala	Thr	180	185	190	
Met	Asp	Ile	Glu	Lys	Cys	Tyr	Asp	Ser	Val	Asn	Arg	Glu	Lys	Leu	Ser	195	200	205	
Thr	Phe	Leu	Lys	Thr	Thr	Lys	Leu	Leu	Ser	Ser	Asp	Phe	Trp	Ile	Met	210	215	220	
Thr	Ala	Gln	Ile	Leu	Lys	Arg	Lys	Asn	225	230									

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2631
- (D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATTTATACTC ATGAAAATCT TATTCGAGTT CATTCAAGAC AAGCTTGACA TTGATCTACA	60
GACCAACAGT ACTTACAAAG AAAATTTAAA ATGTGGTCAC TTCAATGGCC TCGATGAAAT	120
TCTAACTACG TGTTTCGCAC TACCAAATTC AAGAAAAATA GCATTACCAT GCCTTCCTGG	180
TGACTTAAGC CACAAAGCAG TCATTGATCA CTGCATCATT TACCTGTTGA CGGGCGAATT	240
ATACAACAAC GTACTAACAT TTGGCTATAA AATAGCTAGA AATGAAGATG TCAACAATAG	300
TCTTTTTTGC CATTCTGCAA ATGTTAACGT TACGTTACTG AAAGGCGCTG CTTGGAAAAT	360
GTTCCACAGT TTGGTCGGTA CATACGCATT CGTTGATTTA TTGATCAATT ATACAGTAAT	420
TCAATTTAAT GGGCAGTTTT TCACTCAAAT CGTGGGTAAC AGATGTAACG AACCTCATCT	480
GCCGCCCAA TGGGTCCAAC GATCATCCTC ATCATCCGCA ACTGCTGCGC AAATCAAACA	540
ACTTACAGAA CCAGTGACAA ATAAACAATT CTTACACAAG CTCAATATAA ATTCCTCTTC	600
TTTTTTTCCT TATAGCAAGA TCCTTCCTTC ATCATCATCT ATCAAAAAGC TAACTGACTT	660
GAGAGAAGCT ATTTTTCCCA CAAATTTGGT TAAATTCCT CAGAGACTAA AGGTACGAAT	720
TAATTTGACG CTGCAAAAGC TATTAAAGAG ACATAAGCGT TTGAATTACG TTTCTATTTT	780
GAATAGTATT TGCCCACCAT TGAAGGGAC CGTATTGGAC TTGTCGCATT TGAGTAGGCA	840
ATCACCAAAG GAACGAGTCT TGAAATTTAT CATTGTTATT TTACAGAAGT TATTACCCCA	900
AGAAATGTTT GGCTCAAAGA AAAATAAAGG AAAAATTATC AAGAATCTAA ATCTTTTATT	960
AAGTTTACCC TTAAATGGCT ATTTACCATT TGATAGTTTG TTGAAAAAGT TAAGATTAAA	1020
GGATTTTCGG TGGTTGTTCA TTTCTGATAT TTGGTTCACC AAGCACAATT TTGAAAACCT	1080
GAATCAATTG GCGATTTGTT TCATTTCTCG GCTATTTAGA CAACTAATTC CCAAATTAT	1140
ACAGACTTTT TTTTACTGCA CCGAAATATC TTCTACAGTG ACAATTGTTT ACTTTAGACA	1200
TGATACTTGG AATAAACTTA TCACCCCTTT TATCGTAGAA TATTTTAAGA CGTACTTAGT	1260
CGAAAACAAC GTATGTAGAA ACCATAATAG TTACACGTTG TCCAATTTCA ATCATAGCAA	1320
AATGAGGATT ATACCAAAAA AAAGTAATAA TGAGTTCAGG ATTATTGCCA TCCCATGCAG	1380
AGGGGCAGAC GAAGAAGAAT TCACAATTTA TAAGGAGAAT CACAAAAATG CTATCCAGCC	1440
CACTCAAAAA ATTTTAGAAT ACCTAAGAAA CAAAAGGCCG ACTAGTTTTA CTAAAATATA	1500
TTCTCCAACG CAAATAGCTG ACCGTATCAA AGAATTTAAG CAGAGACTTT TAAAGAAATT	1560
TAATAATGTC TTACCAGAGC TTTATTTTAT GAAATTTGAT GTCAAAATCTT GCTATGATTC	1620
CATACCAAGG ATGGAATGTA TGAGGATACT CAAGGATGCG CTAAAAAATG AAAATGGGTT	1680
TTTCGTTAGA TCTCAATATT TCTTCAATAC CAATACAGGT GTATTGAAGT TATTTAATGT	1740
TGTTAACGCT AGCAGAGTAC CAAAACCTTA TGAGCTATAC ATAGATAATG TGAGGACGGT	1800

TCATTTATCA AATCAGGATG TTATAAACGT TGTAGAGATG GAAATATTTA AAACAGCTTT	1860
GTGGGTTGAA GATAAGTGCT ACATTAGAGA AGATGGTCTT TTTCAGGGCT CTAGTTTATC	1920
TGCTCCGATC GTTGATTGG TGTATGACGA TCTTCTGGAG TTTTATAGCG AGTTTAAAGC	1980
CAGTCCTAGC CAGGACACAT TAATTTTAAA ACTGGCTGAC GATTTCTTA TAATATCAAC	2040
AGACCAACAG CAAGTGATCA ATATCAAAAA GCTTGCCATG GGCGGATTTT AAAAATATAA	2100
TGCGAAAGCC AATAGAGACA AAATTTTAGC CGTAAGCTCC CAATCAGATG ATGATACGGT	2160
TATTCAATTT TGTGCAATGC ACATATTTGT TAAAGAATTG GAAGTTTGA AACATTCAAG	2220
CACAATGAAT AATTTCCATA TCCGTTGAA ATCTAGTAAA GGGATATTTT GAAGTTTAAT	2280
AGCGCTGTTT AACACTAGAA TCTCTTATAA AACAATTGAC ACAAATTTAA ATTCAACAAA	2340
CACCGTTCTC ATGCAAATTG ATCATGTTGT AAAGAACATT TCGGAATGTT ATAAATCTGC	2400
TTTTAAGGAT CTATCAATTA ATGTTACGCA AAATATGCAA TTTCATTCTG TCTTACAACG	2460
CATCATTGAA ATGACAGTCA GCGGTTGTCC AATTACGAAA TGTGATCCTT TAATCGAGTA	2520
TGAGGTACGA TTCACCATAT TGAATGGATT TTTGGAAAGC CTATCTTCAA ACACATCAAA	2580
ATTTAAAGAT AATATCATTC TTTTGAGAAA GGAAATTCAA CACTTGCAAG C	2631

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 129 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..129
  - (D) OTHER INFORMATION: /note= "TRT motifs from human"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
 

Ala	Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu
1				5					10					15	
Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu
			20					25					30		
Phe	Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile
			35				40					45			
Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu
			50			55					60				
Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu
65					70					75				80	

Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp  
85 90 95  
Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg  
100 105 110  
Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg  
115 120 125  
Ala

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(959..1216, 1273..1353, 1425..1543, 1595..1857, 1894..2286, 2326..2396, 2436..2705, 2746..2862, 2914..3083, 3125..3309, 3356..3504, 3546..3759, 3797..4046, 4086..4252, 4296..4392, 4435..4597)
- (D) OTHER INFORMATION: /note= "Schizosaccharomyces pombe telomerase catalytic subunit (TRT)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGTACCGATT TACTTTCCTT TCTTCATAAG CTAATTGCTT CCTCGAACGC TCCTAAATCT	60
CTGGAAATAT TTTTACAAGA ACTCAATAAC AATACCAAGT CAAATTCCAA TATGAAGGTG	120
TTATTAGTGA TCGATAATAT TTCTATTTTA TCGGTCGTTA CCAAGTATAA GGACAAAAAG	180
AACAACTTCC TTCCCCCTAA AGACTTTTAC TTTATTAATT TACTTTTCAA ATATATTTCTG	240
GGTTCGCTTA CTTTTAATCG TGGTACTGTT TTAGCTGCTA CTTCTAGCCA ACCGCGTGTT	300
TCTACCCCGT CATTGGATAT AGCTCTTGGA GTAGCTCACA GAAATCCTTA CAAATCTTCT	360
GATGAGACTA TATTAGATTC ATTACAGTCC GTGCATATTC TTAACATGGA GCCTTACACT	420
TTAGATGAGT CACGTCGCAT GATGGAGTAT TTGGTATCAT CCAACGTTTG CCTTGAAAAG	480
GTTGATAATT ATTTGCAAAA TCATGTCCTT AGTGGTGGTA ATCCGCGAAA GTTTTTTGAT	540
GCTTGACACAC GTCTAGCATG ATTGAGATAT TCAAAAATTT CTATCCACTA CAACTCCTTT	600
AACGCGGTTT TATTTTTCTA TTTTCTATTC TCATGTTGTT CCAAATATGT ATCATCTCGT	660
ATTAGGCTTT TTTCCGTTTT ACTCCTGGAA TCGTACCTTT TTTACTATTC CCCCTAATGA	720
ATAATCTAAA TTAGTTTCGC TTATAATTGA TAGTAGTAGA AAGATTGGTG ATTCTACTCG	780



TGTAATGTTA TTAGTTTAAA GATACTTTGC AAAACATTTA TTAGCTATCA TTATATAAAA	840
AAAATCCTAT AATTATAAAT ATTAATCAAT ATTTGCGGTC ACTATTTATT TAAAACGTTA	900
TGATCAGTAG GAACTTTGC ATATATATAG TTATGCTTAA TGGTTACTTG TAACTTGC	958
ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu 1 5 10 15	1006
AAT CAA TAT GTA TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val 20 25 30	1054
TTG AGA GGG TCG CCG GCA AGC TCG TAT AGC AAT ATA TGC GAA CGC TTG Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu 35 40 45	1102
AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT CAT TCG ACT GTA Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val 50 55 60	1150
GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro 65 70 75 80	1198
AAA TGC TCA CAG TCA GAG GTATATATAT TTTTGTTTTG ATTTTTTTTCT Lys Cys Ser Gln Ser Glu 85	1246
ATTCGGGATA GCTAATATAT GGGCAG CTA ATA GCG AAT GTT GTA AAA CAG ATG Leu Ile Ala Asn Val Val Lys Gln Met 90 95	1299
TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA CTG ATG AAA GGG TTT Phe Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe 100 105 110	1347
TCC ATG GTAAGGTATT CTAATTGTGA AATATTTACC TGCAATTACT GTTTCAAAGA Ser Met	1403
GATTGTATTT AACCGATAAA G AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA Asn His Glu Asp Phe Arg Ala Met His Val 115 120	1454
AAC GGA GTA CAA AAT GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA Asn Gly Val Gln Asn Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile 125 130 135	1502
TCT ATA CTT GAG TCA AAA AAT TGG CAA CTT TTG TTA GAA AT Ser Ile Leu Glu Ser Lys Asn Trp Gln Leu Leu Glu Ile 140 145 150	1543
GTAAATACCG GTTAAGATGT TGCGCACTTT GAACAAGACT GACAAGTATA G T ATC Ile	1598
GGC AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG Gly Ser Asp Ala Met His Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu 155 160 165 170	1646

GCT CTT CCA AAT GAC AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT Ala Leu Pro Asn Asp Asn Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe 175 180 185	1694
AAA AAT AAT GTG TTT GAG GAA ACT GTG TCA AAA AAA AGA AAG CGA ACC Lys Asn Asn Val Phe Glu Glu Thr Val Ser Lys Lys Arg Lys Arg Thr 190 195 200	1742
ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA GAA GTT TCC Ile Glu Thr Ser Ile Thr Gln Asn Lys Ser Ala Arg Lys Glu Val Ser 205 210 215	1790
TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC Trp Asn Ser Ile Ser Ile Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser 220 225 230	1838
TAT AAG AAG TTT AAG CAA G GTAACATA CTGTTATCCT TCATAACTAA Tyr Lys Lys Phe Lys Gln 235 240	1887
TTTTAG AT CTA TAT TTT AAC TTA CAC TCT ATT TGT GAT CGG AAC ACA Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr 245 250	1934
GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG CAA TTT GGA CTT ATA Val His Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile 255 260 265 270	1982
AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA TCA Asn Ala Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser 275 280 285	2030
CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT Gln Ser Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile 290 295 300	2078
GAA CAA ACA GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC Glu Gln Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr 305 310 315	2126
AAC CAT TAT TGC CCA TAT ATT GAC ACC CAC GAT GAT GAA AAA ATC CTT Asn His Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu 320 325 330	2174
AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG TTT CTT CGA TCC ATT Ser Tyr Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile 335 340 345 350	2222
CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA TTT Leu Val Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe 355 360 365	2270
GAG ATA ATA TTA AAA G GTATTGTATA AAATTTATTA CCACTAACGA TTTTACCAG AC Glu Ile Ile Leu Lys 370 Asp	2327
CTC GAA ACT TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser Phe Ser Leu His 375 380 385	2375
TAT TTA ATG AGT AAC ATA AAG GTAATATGCC AAATTTTTTTT ACCATTAATT Tyr Leu Met Ser Asn Ile Lys	2426

390		395	
AACAATCAG	ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA AAA AGG TCA		2474
	Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser		
	400 405		
AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT		2522	
Asn Ala Lys Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe			
410 415 420			
GCG GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA		2570	
Ala Glu Phe Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu			
425 430 435 440			
CAA TCT TTT TTT TAT ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT		2618	
Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr			
445 450 455			
GTT TAT TTT AGA AAA GAT ATT TGG AAA CTC TTG TGC CGA CCC TTT ATT		2666	
Val Tyr Phe Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile			
460 465 470			
ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG GTATTTTAAA		2715	
Thr Ser Met Lys Met Glu Ala Phe Glu Lys Ile Asn Glu			
475 480 485			
GTATTTTGTG CAAAAAGCTA ATATTTTCAG AAC AAT GTT AGG ATG GAT ACT CAG		2769	
Asn Asn Val Arg Met Asp Thr Gln			
490			
AAA ACT ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT		2817	
Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn			
495 500 505			
ACC TTT CGT CTC ATT ACG AAT TTA AGA AAA AGA TTC TTA ATA AAG		2862	
Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys			
510 515 520			
GTATTAATTT TTGGTCATCA ATGTACTTTA CTTCTAATCT ATTATTAGCA G ATG GGT		2919	
Met Gly			
525			
TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG		2967	
Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val			
530 535 540			
GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA		3015	
Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro			
545 550 555			
TTT AAC TTG GAG GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT		3063	
Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu			
560 565 570			
CTT AAG CAC CGA ATG TTT GG GTAATTATAT AATGCGCGAT TCCTCATTAT		3113	
Leu Lys His Arg Met Phe Gly			
575 580			
TAATTTTGCA G G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA AAA TCC		3161	
Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser			
585 590			

TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys 595 600 605	3209
AAA CTC AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile His 610 615 620 625	3257
GCA ACA AGT GAC CGA GCT ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe Ser 630 635 640	3305
TAT T GTAAGTTTAT TTTTTCATTG GAATTTTTTA ACAAATTCTT TTTTAG TT Tyr Phe	3357
GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser Met Lys Thr 645 650 655	3405
TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr Lys Ser Ser 660 665 670 675	3453
TCT GAA ATT TTT AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly His Ile Val 680 685 690	3501
AAG GTATACCAAT TGTTGAATTG TAATAACACT AATGAACTA G ATA GGA AAT Lys Ile Gly Asn 695	3554
TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA ATT CTG TCA Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser 700 705 710	3602
TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu 715 720 725	3650
TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp 730 735 740	3698
TTC CTC TTT ATA ACA GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT Phe Leu Phe Ile Thr Val Asn Lys Lys Asp Ala Lys Lys Phe Leu Asn 745 750 755	3746
TTA TCT TTA AGA G GTGAGTTGCT GTCATTCCTA AGTTCTAACC GTTGAAG GA Leu Ser Leu Arg Gly	3798
TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA ATA AAC Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn 765 770 775 780	3846
TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC Phe Glu Asn Ser Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser 785 790 795	3894
AAG AAA AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu	3942

	800	805	810	
GAT ACA TTG TTA GCA TGT CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT				3990
Asp Thr Leu Leu Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser	815	820	825	
ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG AAA TCT TTT TTT TAC AAA				4038
Thr Ser Val Glu Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys	830	835	840	
ATT CTA AG GTATACTGTG TAACTGAATA ATAGCTGACA AATAATCAG A TCG				4089
Ile Leu Arg Ser	845			
AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA				4137
Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser	850	855	860	
AAA TTC AAT TCT TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT				4185
Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys	865	870	875	880
ATG AGA GCA CAA GCA TAC TTA AAA AGG ATG AAG GAT ATA TTT ATT CCC				4233
Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro	885	890	895	
CAA AGA ATG TTC ATA ACG G GTGAGTACTT ATTTTAACTA GAAAAGTCAT				4282
Gln Arg Met Phe Ile Thr	900			
TAATTAACCT TAG AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA				4330
Asp Leu Leu Asn Val Ile Gly Arg Lys Ile Trp Lys	905	910		
AAG TTG GCC GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT				4378
Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu Ser Ser	915	920	925	930
GCA GAA GTC AAA TG GTACGTGTCTG GTCTCGAGAC TTCAGCAATA TTGACACATC				4432
Ala Glu Val Lys Trp	935			
AG G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA CCC TCT TTC AAA				4480
Leu Phe Cys Leu Gly Met Arg Asp Gly Leu Lys Pro Ser Phe Lys	940	945	950	
TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT				4528
Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr Gln Phe Gln Ser Leu Thr	955	960	965	
GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA				4576
Asp Leu Ile Lys Pro Leu Arg Pro Val Leu Arg Gln Val Leu Phe Leu	970	975	980	
CAT AGA AGA ATA GCT GAT TAATGTCATT TTCAATTTAT TATATACATC				4624
His Arg Arg Ile Ala Asp	985			
CTTTATTACT GGTGTCTTAA ACAATATTAT TACTAAGTAT AGCTGACCCC CAAAGCAAGC				4684
ATACTATAGG ATTTCTAGTA AAGTAAAATT AATCTCGTTA TTAGTTTTGA TTGACTTGTC				4744

TTTATCCTTA TACTTTTAAAG AAAGATTGAC AGTGGTTGCT GACTACTGCC CACATGCCCA	4804
TTAAACGGGA GTGGTTAAAC ATTAAAAGTA ATACATGAGG CTAATCTCCT TTCATTTAGA	4864
ATAAGGAAAG TGGTTTTCTA TAATGAATAA TGCCCGCACT AATGCAAAAA GACGAAGATT	4924
ATCTTCTAAA CAAGGGGGAT TAAGCATATC CGAAGGAAAA GAGAGTAATA TACCCAGTGT	4984
TGTTGAAGAA AGCAAGGATA ATTTGGAACA AGCTTCTGCA GATGACAGGC TAAATTTTGG	5044
TGACCGAATT TTGGTAAAAG CCCCAGGTTA TCCATGGTGG CCGGCCTTGC TACTGAGACG	5104
AAAAGAAACT AAGGATAGTT TGAATACTAA TAGCTCATTT AATGTCTTAT ATAAGGTTTT	5164
GTTTTTTCCT GACTTCAATT TTGCATGGGT GAAAAGAAAT AGTGTTAAGC CATTATTGGA	5224
TTCCGAAATA GCCAAATTTT TTGGTTCCTC AAAGCGGAAG TCTAAAGAAC TTATTGAAGC	5284
TTATGAGGCT TCAAAAACCTC CTCCTGATTT AAAGGAGGAA TCTTCCACCG ATGAGGAAAT	5344
GGATAGCTTA TCAGCTGCTG AGGAGAAGCC TAATTTTTTTG CAAAAAAGAA AATATCATTG	5404
GGAGACATCT CTTGATGAAT CAGATGCGGA GAGTATCTCC AGCGGATCCT TGATGTCAAT	5464
AACTTCTATT TCTGAAATGT ATGGTCCTAC TGTCGCTTCG ACTTCTCGTA GCTCTACGCA	5524
GTTAAGTGAC CAAAGGTACC	5544

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu	1	5	10	15
Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val	20	25	30	
Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu	35	40	45	
Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val	50	55	60	
Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro	65	70	75	80
Lys Cys Ser Gln Ser Glu Leu Ile Ala Asn Val Val Lys Gln Met Phe	85	90	95	
Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe Ser	100	105	110	
Met Asn His Glu Asp Phe Arg Ala Met His Val Asn Gly Val Gln Asn				

115					120					125					
Asp	Leu	Val	Ser	Thr	Phe	Pro	Asn	Tyr	Leu	Ile	Ser	Ile	Leu	Glu	Ser
130						135					140				
Lys	Asn	Trp	Gln	Leu	Leu	Leu	Glu	Ile	Ile	Gly	Ser	Asp	Ala	Met	His
145					150					155					160
Tyr	Leu	Leu	Ser	Lys	Gly	Ser	Ile	Phe	Glu	Ala	Leu	Pro	Asn	Asp	Asn
				165					170					175	
Tyr	Leu	Gln	Ile	Ser	Gly	Ile	Pro	Leu	Phe	Lys	Asn	Asn	Val	Phe	Glu
			180					185					190		
Glu	Thr	Val	Ser	Lys	Lys	Arg	Lys	Arg	Thr	Ile	Glu	Thr	Ser	Ile	Thr
		195					200					205			
Gln	Asn	Lys	Ser	Ala	Arg	Lys	Glu	Val	Ser	Trp	Asn	Ser	Ile	Ser	Ile
	210					215					220				
Ser	Arg	Phe	Ser	Ile	Phe	Tyr	Arg	Ser	Ser	Tyr	Lys	Lys	Phe	Lys	Gln
225					230					235					240
Asp	Leu	Tyr	Phe	Asn	Leu	His	Ser	Ile	Cys	Asp	Arg	Asn	Thr	Val	His
				245					250					255	
Met	Trp	Leu	Gln	Trp	Ile	Phe	Pro	Arg	Gln	Phe	Gly	Leu	Ile	Asn	Ala
			260					265					270		
Phe	Gln	Val	Lys	Gln	Leu	His	Lys	Val	Ile	Pro	Leu	Val	Ser	Gln	Ser
		275					280					285			
Thr	Val	Val	Pro	Lys	Arg	Leu	Leu	Lys	Val	Tyr	Pro	Leu	Ile	Glu	Gln
	290					295					300				
Thr	Ala	Lys	Arg	Leu	His	Arg	Ile	Ser	Leu	Ser	Lys	Val	Tyr	Asn	His
305					310					315				320	
Tyr	Cys	Pro	Tyr	Ile	Asp	Thr	His	Asp	Asp	Glu	Lys	Ile	Leu	Ser	Tyr
				325					330					335	
Ser	Leu	Lys	Pro	Asn	Gln	Val	Phe	Ala	Phe	Leu	Arg	Ser	Ile	Leu	Val
			340					345					350		
Arg	Val	Phe	Pro	Lys	Leu	Ile	Trp	Gly	Asn	Gln	Arg	Ile	Phe	Glu	Ile
		355					360					365			
Ile	Leu	Lys	Asp	Leu	Glu	Thr	Phe	Leu	Lys	Leu	Ser	Arg	Tyr	Glu	Ser
	370					375					380				
Phe	Ser	Leu	His	Tyr	Leu	Met	Ser	Asn	Ile	Lys	Ile	Ser	Glu	Ile	Glu
385					390					395					400
Trp	Leu	Val	Leu	Gly	Lys	Arg	Ser	Asn	Ala	Lys	Met	Cys	Leu	Ser	Asp
				405					410					415	
Phe	Glu	Lys	Arg	Lys	Gln	Ile	Phe	Ala	Glu	Phe	Ile	Tyr	Trp	Leu	Tyr
			420					425					430		
Asn	Ser	Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	Phe	Tyr	Ile	Thr	Glu
		435					440					445			

Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys Asp Ile Trp  
 450 455 460  
 Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met Glu Ala Phe  
 465 470 475 480  
 Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr  
 485 490 495  
 Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg  
 500 505 510  
 Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn  
 515 520 525  
 Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val Ala Ser  
 530 535 540  
 Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro Phe Asn  
 545 550 555 560  
 Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu Leu Lys  
 565 570 575  
 His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys  
 580 585 590  
 Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys  
 595 600 605  
 Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile  
 610 615 620  
 His Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe  
 625 630 635 640  
 Ser Tyr Phe Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser  
 645 650 655  
 Met Lys Thr Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr  
 660 665 670  
 Lys Ser Ser Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly  
 675 680 685  
 His Ile Val Lys Ile Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile  
 690 695 700  
 Pro Gln Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu  
 705 710 715 720  
 Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val  
 725 730 735  
 Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys  
 740 745 750  
 Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His  
 755 760 765  
 Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn Ser  
 770 775 780



Asn	Gly	Ile	Ile	Asn	Asn	Thr	Phe	Phe	Asn	Glu	Ser	Lys	Lys	Arg	Met	785	790	795	800
Pro	Phe	Phe	Gly	Phe	Ser	Val	Asn	Met	Arg	Ser	Leu	Asp	Thr	Leu	Leu	805	810		815
Ala	Cys	Pro	Lys	Ile	Asp	Glu	Ala	Leu	Phe	Asn	Ser	Thr	Ser	Val	Glu	820	825		830
Leu	Thr	Lys	His	Met	Gly	Lys	Ser	Phe	Phe	Tyr	Lys	Ile	Leu	Arg	Ser	835	840		845
Ser	Leu	Ala	Ser	Phe	Ala	Gln	Val	Phe	Ile	Asp	Ile	Thr	His	Asn	Ser	850	855		860
Lys	Phe	Asn	Ser	Cys	Cys	Asn	Ile	Tyr	Arg	Leu	Gly	Tyr	Ser	Met	Cys	865	870	875	880
Met	Arg	Ala	Gln	Ala	Tyr	Leu	Lys	Arg	Met	Lys	Asp	Ile	Phe	Ile	Pro	885	890		895
Gln	Arg	Met	Phe	Ile	Thr	Asp	Leu	Leu	Asn	Val	Ile	Gly	Arg	Lys	Ile	900	905		910
Trp	Lys	Lys	Leu	Ala	Glu	Ile	Leu	Gly	Tyr	Thr	Ser	Arg	Arg	Phe	Leu	915	920		925
Ser	Ser	Ala	Glu	Val	Lys	Trp	Leu	Phe	Cys	Leu	Gly	Met	Arg	Asp	Gly	930	935	940	
Leu	Lys	Pro	Ser	Phe	Lys	Tyr	His	Pro	Cys	Phe	Glu	Gln	Leu	Ile	Tyr	945	950	955	960
Gln	Phe	Gln	Ser	Leu	Thr	Asp	Leu	Ile	Lys	Pro	Leu	Arg	Pro	Val	Leu	965	970		975
Arg	Gln	Val	Leu	Phe	Leu	His	Arg	Arg	Ile	Ala	Asp					980	985		

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod\_base= OTHER  
/note= "N = guanosine modified by a biotin group"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

NCCTATTTTGT TYTAYNNNAC NGA

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Phe Phe Tyr Xaa Thr Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCAGATATNA DNARRAARTC RTC

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Phe, Ile or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Asp Asp Phe Leu Xaa Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACAATGMGNH TNHTNCCNAA RAA

23

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2..3
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Leu or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Arg Xaa Xaa Pro Lys Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ACGAATCKNG GDATNSWRTC RTARCA

26

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Cys Tyr Asp Ser Ile Pro Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAATTCTCRT ARCANSWYTT DATRTC

26

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Asp Ile Lys Ser Cys Tyr Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 269 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GATTACTCCC GAAGAAAGGA TCTTTCCGTC CAATCATGAC TTTCTTAAGA AAGGACAAGC	60
AAAAAATAT TAAGTTAAAT CTAAATTAAA TTCTAATGGA TAGCCAACCT GTGTTTAGGA	120
ATTTAAAAGA CATGCTGGGA TAAAAGATAG GATACTCAGT CTTTGATAAT AAACAAATTT	180
CAGAAAAATT TGCCTAATTC ATAGAGAAAT GGAAAAATAA AGGAAGACCT CAGCTATATT	240
ATGTCACTCT AGACATAAAG ACTTGCTAC	269

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 474 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAACACAAGG AAGGAAGTCA AATATTCTAT TACCGTAAAC CAATATGGAA ATTAGTGAGT	60
AAATTAAC TA TGTCAAAGT AAGAATTTAG TTTTCTGAAA AGAATAAATA AATGAAAAAT	120
AATTTTTATC AAAAAATTTA GCTTGAAGAG GAGAATTTGG AAAAAGTTGA AGAAAAATTG	180
ATACCAGAAG ATTCATTTTA GAAATACCCT CAAGGAAAGC TAAGGATTAT ACCTAAAAAA	240
GGATCTTTCC GTCCAATCAT GACTTTCTTA AGAAAGGACA AGCAAAAAAA TATTAAGTTA	300
AATCTAAATT AAATTCTAAT GGATAGCCAA CTTGTGTTTA GGAATTTAAA AGACATGCTG	360
GGATAAAAGA TAGGATACTC AGTCTTTGAT AATAAACAAA TTTCAGAAAA ATTTGCCTAA	420
TTCATAGAGA AATGGAAAAA TAAAGGAAGA CCTCAGCTAT ATTATGTCAC TCTA	474

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 158 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Lys His Lys Glu Gly Ser Gln Ile Phe Tyr Tyr Arg Lys Pro Ile Trp	1 5 10 15
Lys Leu Val Ser Lys Leu Thr Ile Val Lys Val Arg Ile Gln Phe Ser	20 25 30
Glu Lys Asn Lys Gln Met Lys Asn Asn Phe Tyr Gln Lys Ile Gln Leu	35 40 45
Glu Glu Glu Asn Leu Glu Lys Val Glu Glu Lys Leu Ile Pro Glu Asp	50 55 60
Ser Phe Gln Lys Tyr Pro Gln Gly Lys Leu Arg Ile Ile Pro Lys Lys	65 70 75 80
Gly Ser Phe Arg Pro Ile Met Thr Phe Leu Arg Lys Asp Lys Gln Lys	85 90 95
Asn Ile Lys Leu Asn Leu Asn Gln Ile Leu Met Asp Ser Gln Leu Val	100 105 110
Phe Arg Asn Leu Lys Asp Met Leu Gly Gln Lys Ile Gly Tyr Ser Val	115 120 125
Phe Asp Asn Lys Gln Ile Ser Glu Lys Phe Ala Gln Phe Ile Glu Lys	

130	135	140
Trp Lys Asn Lys Gly Arg Pro Gln Leu Tyr Tyr Val Thr Leu		
145	150	155

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Phe	Phe	Tyr	Cys	Thr	Glu	Ile	Ser	Ser	Thr	Val	Thr	Ile	Val	Tyr	Phe
1				5					10					15	
Arg	His	Asp	Thr	Trp	Asn	Lys	Leu	Ile	Thr	Pro	Phe	Ile	Val	Glu	Tyr
		20					25						30		
Phe	Lys	Thr	Tyr	Leu	Val	Glu	Asn	Asn	Val	Cys	Arg	Asn	His	Asn	Ser
		35					40					45			
Tyr	Thr	Leu	Ser	Asn	Phe	Asn	His	Ser	Lys	Met	Arg	Ile	Ile	Pro	Lys
		50					55				60				
Lys	Ser	Asn	Asn	Glu	Phe	Arg	Ile	Ile	Ala	Ile	Pro	Cys	Arg	Gly	Ala
65					70				75					80	
Asp	Glu	Glu	Glu	Phe	Thr	Ile	Tyr	Lys	Glu	Asn	His	Lys	Asn	Ala	Ile
				85					90					95	
Gln	Pro	Thr	Gln	Lys	Ile	Leu	Glu	Tyr	Leu	Arg	Asn	Lys	Arg	Pro	Thr
			100					105					110		
Ser	Phe	Thr	Lys	Ile	Tyr	Ser	Pro	Thr	Gln	Ile	Ala	Asp	Arg	Ile	Lys
		115					120					125			
Glu	Phe	Lys	Gln	Arg	Leu	Leu	Lys	Lys	Phe	Asn	Asn	Val	Leu	Pro	Glu
		130				135						140			
Leu	Tyr	Phe	Met	Lys	Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp			
145					150					155					

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 155 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Phe	Phe	Tyr	Val	Thr	Glu	Gln	Gln	Lys	Ser	Tyr	Ser	Lys	Thr	Tyr	Tyr
1				5					10					15	
Tyr	Arg	Lys	Asn	Ile	Trp	Asp	Val	Ile	Met	Lys	Met	Ser	Ile	Ala	Asp
			20					25					30		
Leu	Lys	Lys	Glu	Thr	Leu	Ala	Glu	Val	Gln	Glu	Lys	Glu	Val	Glu	Glu
		35					40					45			
Trp	Lys	Lys	Ser	Leu	Gly	Phe	Ala	Pro	Gly	Lys	Leu	Arg	Leu	Ile	Pro
	50					55					60				
Lys	Lys	Thr	Thr	Phe	Arg	Pro	Ile	Met	Thr	Phe	Asn	Lys	Lys	Ile	Val
65					70					75					80
Asn	Ser	Asp	Arg	Lys	Thr	Thr	Lys	Leu	Thr	Thr	Asn	Thr	Lys	Leu	Leu
				85					90					95	
Asn	Ser	His	Leu	Met	Leu	Lys	Thr	Leu	Lys	Asn	Arg	Met	Phe	Lys	Asp
			100					105					110		
Pro	Phe	Gly	Phe	Ala	Val	Phe	Asn	Tyr	Asp	Asp	Val	Met	Lys	Lys	Tyr
		115					120					125			
Glu	Glu	Phe	Val	Cys	Lys	Trp	Lys	Gln	Val	Gly	Gln	Pro	Lys	Leu	Phe
	130					135					140				
Phe	Ala	Thr	Met	Asp	Ile	Glu	Lys	Cys	Tyr	Asp					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 158 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Lys	His	Lys	Glu	Gly	Ser	Gln	Ile	Phe	Tyr	Tyr	Arg	Lys	Pro	Ile	Trp
1				5					10					15	
Lys	Leu	Val	Ser	Lys	Leu	Thr	Ile	Val	Lys	Val	Arg	Ile	Gln	Phe	Ser
			20					25					30		
Glu	Lys	Asn	Lys	Gln	Met	Lys	Asn	Asn	Phe	Tyr	Gln	Lys	Ile	Gln	Leu
		35				40						45			
Glu	Glu	Glu	Asn	Leu	Glu	Lys	Val	Glu	Glu	Lys	Leu	Ile	Pro	Glu	Asp
	50					55					60				
Ser	Phe	Gln	Lys	Tyr	Pro	Gln	Gly	Lys	Leu	Arg	Ile	Ile	Pro	Lys	Lys
65				70					75					80	
Gly	Ser	Phe	Arg	Pro	Ile	Met	Thr	Phe	Leu	Arg	Lys	Asp	Lys	Gln	Lys
				85					90					95	

Asn Ile Lys Leu Asn Leu Asn Gln Ile Leu Met Asp Ser Gln Leu Val  
100 105 110  
Phe Arg Asn Leu Lys Asp Met Leu Gly Gln Lys Ile Gly Tyr Ser Val  
115 120 125  
Phe Asp Asn Lys Gln Ile Ser Glu Lys Phe Ala Gln Phe Ile Glu Lys  
130 135 140  
Trp Lys Asn Lys Gly Arg Pro Gln Leu Tyr Tyr Val Thr Leu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala  
1 5 10 15  
Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp  
20 25 30  
Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys  
35 40 45  
Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr  
50 55 60  
Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu  
65 70 75 80  
Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val  
85 90 95  
Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys  
100 105 110  
Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu  
115 120 125  
Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn  
130 135 140  
Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr  
145 150 155 160  
Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe  
165 170 175  
Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp  
180 185 190



Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys  
 195 200 205  
 Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn  
 210 215 220  
 Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile  
 225 230 235 240  
 Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His  
 245 250 255  
 Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln  
 260 265 270  
 Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu  
 275 280 285  
 Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys  
 290 295 300  
 Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu  
 305 310 315 320  
 Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr  
 325 330 335  
 Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr  
 340 345 350  
 Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile  
 355 360 365  
 Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys  
 370 375 380  
 Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys  
 385 390 395 400  
 Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln  
 405 410 415  
 Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile  
 420 425 430  
 Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val  
 435 440 445  
 Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr  
 450 455 460  
 Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys  
 465 470 475 480  
 Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu  
 485 490 495  
 Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys  
 500 505 510  
 Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe  
 515 520 525

Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr  
 530 535 540  
 Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn  
 545 550 555 560  
 Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp  
 565 570 575  
 Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly  
 580 585 590  
 Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp  
 595 600 605  
 Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu  
 610 615 620  
 Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys  
 625 630 635 640  
 Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys  
 645 650 655  
 Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln  
 660 665 670  
 Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn  
 675 680 685  
 Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys  
 690 695 700  
 Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr  
 705 710 715 720  
 Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln  
 725 730 735  
 Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu  
 740 745 750  
 Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu  
 755 760 765  
 Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu  
 770 775 780  
 Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile  
 785 790 795 800  
 Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln  
 805 810 815  
 Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp  
 820 825 830  
 Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly  
 835 840 845  
 Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu  
 850 855 860

Arg	Ile	Glu	Gly	Ile	Leu	Cys	Thr	Leu	Asn	Leu	Asn	Met	Gln	Thr	Lys
865					870					875					880
Lys	Ala	Ser	Met	Trp	Leu	Lys	Lys	Lys	Leu	Lys	Ser	Phe	Leu	Met	Asn
				885					890					895	
Asn	Ile	Thr	His	Tyr	Phe	Arg	Lys	Thr	Ile	Thr	Thr	Glu	Asp	Phe	Ala
			900					905					910		
Asn	Lys	Thr	Leu	Asn	Lys	Leu	Phe	Ile	Ser	Gly	Gly	Tyr	Lys	Tyr	Met
		915					920					925			
Gln	Cys	Ala	Lys	Glu	Tyr	Lys	Asp	His	Phe	Lys	Lys	Asn	Leu	Ala	Met
	930					935					940				
Ser	Ser	Met	Ile	Asp	Leu	Glu	Val	Ser	Lys	Ile	Ile	Tyr	Ser	Val	Thr
945					950					955					960
Arg	Ala	Phe	Phe	Lys	Tyr	Leu	Val	Cys	Asn	Ile	Lys	Asp	Thr	Ile	Phe
				965					970					975	
Gly	Glu	Glu	His	Tyr	Pro	Asp	Phe	Phe	Leu	Ser	Thr	Leu	Lys	His	Phe
			980					985					990		
Ile	Glu	Ile	Phe	Ser	Thr	Lys	Lys	Tyr	Ile	Phe	Asn	Arg	Val	Cys	
		995					1000					1005			

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGAAGGCAC TGTTTCAGCG

19

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTGGATGATT TCTTGTGG

19

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGCTCCTGC GTTTGGTGG

19

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTGGACACTC AGCCCTTGG

19

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGCAGGTGTG CTGGACACT

19

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TTTGATGATG CTGGCGATG

19

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGGGCTCGTC TTCTACAGG

19

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CAGCAGGAGG ATCTTGTAG

19

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TGACCCCAGG AGTGGCAGC

19

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCAAGCTGAC TCGACACCG

19

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGGCGTGACA GGGCTGC

17

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCTGAAGGCT GAGTGTCC

18

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TAGTCCATGT TCACAATCG

19

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2171 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 22..1716
- (D) OTHER INFORMATION: /note= "EcoRI-NotI insert of clone 712562 encoding 63 kDa

telomerase protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCCAAGTTCC	TGCACTGGCT	GATGAGTGTG	TACGTCGTCG	AGCTGCTCAG	GTCTTTCTTT	60
TATGTCACGG	AGACCACGTT	TCAAAAGAAC	AGGCTCTTTT	TCTACCGGAA	GAGTGTCTGG	120
AGCAAGTTGC	AAAGCATTGG	AATCAGACAG	CACTTGAAGA	GGGTGCAGCT	GCGGGAGCTG	180
TCGGAAGCAG	AGGTCAGGCA	GCATCGGGAA	GCCAGGCCCC	CCCTGCTGAC	GTCCAGACTC	240
CGCTTCATCC	CCAAGCCTGA	CGGGCTGCGG	CCGATTGTGA	ACATGGACTA	CGTCGTGGGA	300
GCCAGAACGT	TCCGCAGAGA	AAAGARGGCC	GAGCGTCTCA	CCTCGAGGGT	GAAGGCACTG	360
TTCAGCGTGC	TCAACTACGA	GCGGGCGCGG	CGCCCCGGCC	TCCTGGGCGC	CTCTGTGCTG	420
GGCCTGGACG	ATATCCACAG	GGCCTGGCGC	ACCTTCGTGC	TGCGTGTGCG	GGCCCAGGAC	480
CCGCCGCTG	AGCTGTACTT	TGTCAAGGTG	GATGTGACGG	GCGCGTACGA	CACCATCCCC	540
CAGGACAGGC	TCACGGAGGT	CATCGCCAGC	ATCATCAAAC	CCCAGAACAC	GTA CTGCGTG	600
CGTCGGTATG	CCGTGGTCCA	GAAGGCCGCC	ATGGGCACGT	CCGCAAGGCC	TTCAAGAGCC	660
ACGTCTTACG	TCCAGTGCCA	GGGGATCCCG	CAGGGCTCCA	TCCTCTCCAC	GCTGCTCTGC	720
AGCCTGTGCT	ACGGCGACAT	GGAGAACAAG	CTGTTTGCGG	GGATTGCGCG	GGACGGGCTG	780
CTCCTGCGTT	TGGTGGATGA	TTTCTTGTTG	GTGACACCTC	ACCTCACCCA	CGCGAAAACC	840
TTCTCAGGA	CCCTGGTCCG	AGGTGTCCCT	GAGTATGGCT	GCGTGGTGAA	CTTGCGGAAG	900
ACAGTGGTGA	ACTTCCCTGT	AGAAGACGAG	GCCCTGGGTG	GCACGGCTTT	TGTTCAAGATG	960
CCGGCCCACG	GCCTATTCCC	CTGGTGCGGC	CTGCTGCTGG	ATACCCGGAC	CCTGGAGGTG	1020
CAGAGCGACT	ACTCCAGCTA	TGCCCCGACC	TCCATCAGAG	CCAGTCTCAC	CTTCAACCGC	1080
GGCTTCAAGG	CTGGGAGGAA	CATGCGTCGC	AAACTCTTTG	GGGTCTTGCG	GCTGAAGTGT	1140
CACAGCCTGT	TTCTGGATTT	GCAGGTGAAC	AGCCTCCAGA	CGGTGTGCAC	CAACATCTAC	1200
AAGATCCTCC	TGCTGCAGGC	GTACAGGTTT	CACGCATGTG	TGCTGCAGCT	CCCATTTTCA	1260
CAGCAAGTTT	GGAAGAACCC	ACATTTTTC	TGCGCGTCAT	CTCTGACACG	GCTCCCTCTG	1320
CTACTCCATC	CTGAAAGCCA	AGAACGCAGG	GATGTCGCTG	GGGGCCAAGG	GCGCCGCCGG	1380
CCCTCTGCCC	TCCGAGGCCG	TGCAGTGGCT	GTGCCACCAA	GCATTCCCTG	TCAAGCTGAC	1440
TCGACACCGT	GTCACCTACG	TGCCACTCCT	GGGGTCACTC	AGGACAGCCC	AGACGCAGCT	1500
GAGTCGGAAG	CTCCCGGGGA	CGACGCTGAC	TGCCCTGGAG	GCCGCAGCCA	ACCCGGCACT	1560
GCCCTCAGAC	TTCAAGACCA	TCCTGGACTG	ATGGCCACCC	GCCCACAGCC	AGGCCGAGAG	1620
CAGACACCAG	CAGCCCTGTC	ACGCCGGGCT	TATACGTCCC	AGGGAGGGAG	GGGCGGCCCA	1680
CACCCAGGCC	TGCACCGCTG	GGAGTCTGAG	GCCTGAGTGA	GTGTTTGGCC	GAGGCCTGCA	1740

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TGTCGGCTG AAGGCTGAGT GTCCGGCTGA GGCCTGAGCG AGTGTCCAGC CAAGGGCTGA      1800
GTGTCCAGCA CACCTGCGTT TTCACTTCCC CACAGGCTGG CGTTCGGTCC ACCCCAGGGC      1860
CAGCTTTTCC TCACCAGGAG CCCGGCTTCC ACTCCCCACA TAGGAATAGT CCATCCCCAG      1920
ATTTCGCCATT GTTCACCCTT CGCCCTGCCT TCCTTTGCCT TCCACCCCCA CCATTCAGGT      1980
GGAGACCCTG AGAAGGACCC TGGGAGCTTT GGGAAATTGG AGTGACCAA GGTGTGCCCT      2040
GTACACAGGC GAGGACCCTG CACCTGGATG GGGGTCCCTG TGGGTCAAAT TGGGGGGAGG      2100
TGCTGTGGGA GTAAAATACT GAATATATGA GTTTTTCAGT TTTGGAAAAA AAAAAAAAAA      2160
AAAAAAAAA A                                                                2171

```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..564
- (D) OTHER INFORMATION: /note= "63 kDa telomerase protein  
encoded by ORF of EcoRI-NotI insert of  
clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```

Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr
1           5           10           15
Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val
20          25          30
Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val
35          40          45
Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala
50          55          60
Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp
65          70          75          80
Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr
85          90          95
Phe Arg Arg Glu Lys Xaa Ala Glu Arg Leu Thr Ser Arg Val Lys Ala
100         105         110
Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu
115        120        125

```



Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr  
 130 135 140  
 Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe  
 145 150 155 160  
 Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg  
 165 170 175  
 Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys  
 180 185 190  
 Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala Met Gly Thr Ser Ala  
 195 200 205  
 Arg Pro Ser Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln  
 210 215 220  
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met  
 225 230 235 240  
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg  
 245 250 255  
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys  
 260 265 270  
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val  
 275 280 285  
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala  
 290 295 300  
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro  
 305 310 315 320  
 Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp  
 325 330 335  
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn  
 340 345 350  
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val  
 355 360 365  
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser  
 370 375 380  
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala  
 385 390 395 400  
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val  
 405 410 415  
 Trp Lys Asn Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg Leu Pro  
 420 425 430  
 Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp Val Ala Gly Gly  
 435 440 445  
 Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg Gly Arg Ala Val Ala Val  
 450 455 460

Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro Cys His Leu Arg  
 465 470 475 480

Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala Ala Glu Ser Glu  
 485 490 495

Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg Ser Gln Pro Gly  
 500 505 510

Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met Ala Thr Arg Pro  
 515 520 525

Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser Arg Arg Ala Tyr  
 530 535 540

Thr Ser Gln Gly Gly Arg Gly Gly Pro His Pro Gly Leu His Arg Trp  
 545 550 555 560

Glu Ser Glu Ala

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCAGTGAGCA GAGTGACGAG GACTCGAGCT CAAGCTTTTTT TTTTTTTTTT

50

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CCAGTGAGCA GAGTGACG

18

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:  
GAGGACTCGA GCTCAAGC 18

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:  
CACTGATCCT TTCTTTTTCG TAAACGATAG GT 32

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:  
CATCAATCAA ATCTTCCATA TAGAAATGAC A 31

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:  
(A) NAME/KEY: modified\_base  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /mod\_base= OTHER  
/note= "N = 5'-phosphorylated guanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:  
NGGCCGTGTT GGCCTAGTTC TCTGCTC 27

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAGGAGGAGA AGAGCAGAGA ACTAGGCCAA CACGCCCC

38

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTGTCATTTT TATATGGAAG ATTTGATTGA TG

32

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ACCTATCGTT TACGAAAAAG AAAGGATCAG TG

32

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAGTGACATA ATATACGTGA

20

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe  
1                      5                      10                      15  
Tyr Arg Lys Ser Val Trp Ser Lys  
                    20

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser Glu Ala Glu  
1                      5                      10                      15  
Val Arg Gln His Arg Glu Ala  
                    20

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg  
1                      5                      10                      15  
Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu  
                    20                      25

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

(2) INFORMATION FOR SEQ ID NO:116:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

(2) INFORMATION FOR SEQ ID NO:117:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

(2) INFORMATION FOR SEQ ID NO:118:

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Gln Thr Lys Gly Ile Pro Gln Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

NGTNATDARD ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Asp Asp Tyr Leu Leu Ile Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe  
1 5 10 15  
Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu  
20 25 30  
Ser Met Asn Pro Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr  
35 40 45  
Asp Asp Tyr Leu Leu Ile Thr  
50 55

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile  
1 5 10 15  
Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg  
20 25 30  
Val Val

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile Val Asp Leu  
1 5 10 15  
Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys Ala Ser Pro  
20 25 30  
Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile  
35 40 45  
Ser



(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Gln Lys Val Gly Ile Pro Gln Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CAAAAAGTTG GTATCCCTCA GGG

23

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 146 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

AGACCAAAGG AATTCCATCA GGCTCAATTC TGTCATCTTT TTTGTGTCAT TTCTATATGG 60

AAGATTTGAT TGATGAATAC CTATCGTTTA CGAAAAAGAA AGGATCAGTG TTGTTACGAG 120

TAGTCGACGA CTACCTCCTC ATCACC 146

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Lys Gly Ile Pro Ser Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe  
1                      5                      10                      15  
Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys  
                    20                      25                      30  
Gly Ser Val Leu Leu Arg Val Val Asp Asp Tyr Leu Leu Ile Thr  
                    35                      40                      45

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GACGATTTCC TCTTTATAAC A

21

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Asp Phe Leu Phe Ile Thr  
1                      5

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

AAAAAAAAAA AAAAAA

16

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

TTTTTTTTTT TTTTTT

17

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif 0 peptide from Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Trp	Leu	Tyr	Asn	Ser	Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	Phe	Tyr
1				5				10						15	
Ile	Thr	Glu	Ser	Ser	Asp	Leu	Arg	Asn	Arg	Thr	Val	Tyr	Phe	Arg	Lys
			20					25					30		
Asp	Ile	Trp													
															35

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Ala	Val	Ile	Arg	Leu	Leu	Pro	Lys	Lys	Asn	Thr	Phe	Arg	Leu	Ile	Thr
1				5					10				15		

Asn Leu Arg Lys Arg Phe  
20

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..26  
(D) OTHER INFORMATION: /note= "motif 3(A) peptide from  
Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile  
1 5 10 15  
Lys Gln Asp Leu Met Phe Arg Ile Val Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..32  
(D) OTHER INFORMATION: /note= "motif 4(B') peptide from  
Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe  
1 5 10 15  
Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe  
20 25 30

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..49  
(D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from  
Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys  
1 5 10 15  
Lys Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys  
20 25 30  
His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn  
35 40 45  
Ser

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..34  
(D) OTHER INFORMATION: /note= "motif 0 peptide from  
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr  
1 5 10 15  
Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp  
20 25 30  
Thr Trp

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids  
(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from  
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```
Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu Phe Arg Ile
1           5           10           15

Ile Ala Ile Pro Cys Arg Gly Ala Asp
          20           25
```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile
1           5           10           15

Pro Arg Met Glu Cys Met Arg Ile Leu Lys
          20           25
```

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide

(B) LOCATION: 1..32  
(D) OTHER INFORMATION: /note= "motif 4(B') peptide from  
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro  
1 5 10 15

Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe  
20 25 30

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..49  
(D) OTHER INFORMATION: /note= "motif 5(C) peptide from  
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln  
1 5 10 15

Gln Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys  
20 25 30

Tyr Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala Val Ser Ser Gln  
35 40 45

Ser

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..35  
(D) OTHER INFORMATION: /note= "motif 0 peptide from  
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr  
1                   5                   10                   15  
Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys  
                  20                   25                   30  
Asn Ile Trp  
            35

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..23
  - (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met  
1                   5                   10                   15  
Thr Phe Asn Lys Lys Ile Val  
            20

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..26
  - (D) OTHER INFORMATION: /note= "motif 3(A) peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val  
1                   5                   10                   15



Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys  
 20 25

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "motif 4(B') peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile  
 1 5 10 15  
 Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu  
 1 5 10 15  
 Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu  
 20 25 30  
 Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro Leu  
 35 40 45  
 Ser

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..22
  - (D) OTHER INFORMATION: /note= "motif 1 peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln  
1                    5                    10                    15  
  
Lys Ser Tyr Ser Lys Thr  
                    20

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..30
  - (D) OTHER INFORMATION: /note= "motif 0 peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys  
1                    5                    10                    15  
  
Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val  
                    20                    25                    30

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..27

(D) OTHER INFORMATION

Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser  
1 5 10 15

(B) TYPE: amino acid

(C) STRANDEDNESS:

(ix) FEATURE:

(B) LOCATION: 1..27

(D) OTHER INFORMATION

Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys  
1 5 10 15

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 22

95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile  
1                   5                   10                   15  
Thr Thr Gln Glu Asn Asn  
                  20

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from  
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu  
1                   5                   10                   15

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from  
Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser  
1                   5                   10                   15  
Asp Leu Arg Asn Arg Thr  
                  20

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..30
  - (D) OTHER INFORMATION: /note= "motif 0 peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Gln	Lys	Thr	Thr	Leu	Pro	Pro	Ala	Val	Ile	Arg	Leu	Leu	Pro	Lys	Lys
1				5					10					15	
Asn	Thr	Phe	Arg	Leu	Ile	Thr	Asn	Leu	Arg	Lys	Arg	Phe	Leu		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..27
  - (D) OTHER INFORMATION: /note= "motif A peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Arg	Lys	Lys	Tyr	Phe	Val	Arg	Ile	Asp	Ile	Lys	Ser	Cys	Tyr	Asp	Arg
1				5					10					15	
Ile	Lys	Gln	Asp	Leu	Met	Phe	Arg	Ile	Val	Lys					
			20					25							

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile  
1                   5                   10                   15  
Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu  
                 20                   25

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif C peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile  
1                   5                   10                   15  
Thr Val Asn Lys Lys Asp  
                 20

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His Asn Phe Ser Thr  
 1                      5                      10                      15

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from  
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr Glu Ile Ser  
 1                      5                      10                      15  
 Ser Thr Val Thr Ile Val  
                     20

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "motif 0 peptide from  
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys  
 1                      5                      10                      15  
 Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp  
                     20                      25                      30

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from  
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Pro	Glu	Leu	Tyr	Phe	Met	Lys	Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp	Ser
1					5				10					15	
Ile	Pro	Arg	Met	Glu	Cys	Met	Arg	Ile	Leu	Lys					
			20					25							

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from  
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Glu	Asp	Lys	Cys	Tyr	Ile	Arg	Glu	Asp	Gly	Leu	Phe	Gln	Gly	Ser	Ser
1					5				10					15	
Leu	Ser	Ala	Pro	Ile	Val	Asp	Leu	Val	Tyr	Asp					
					20			25							

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide



(B) LOCATION: 1..22  
(D) OTHER INFORMATION: /note= "motif C peptide from  
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile  
1 5 10 15  
Ser Thr Asp Gln Gln Gln  
20

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..15  
(D) OTHER INFORMATION: /note= "motif D peptide from  
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..22  
(D) OTHER INFORMATION: /note= "motif 1 peptide from human  
telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr  
1 5 10 15  
Phe Gln Lys Asn Arg Leu  
20

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..30  
 (D) OTHER INFORMATION: /note= "motif 0 peptide from human  
telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Ala Arg Pro Ala Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
1                  5                  10                  15  
Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly  
                  20                  25                  30

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..27  
 (D) OTHER INFORMATION: /note= "motif A peptide from human  
telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr  
1                  5                  10                  15  
Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala  
                  20                  25

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..27

(D) OTHER INFORMATION: /note= "motif B peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile  
1                   5                   10                   15

Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly  
20                   25

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..22

(D) OTHER INFORMATION: /note= "motif C peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val  
1                   5                   10                   15

Thr Pro His Leu Thr His  
20

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..15

(D) OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	Val
1				5					10					15